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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlp
-O-/Cgn2_1/USPTO_spoo1/US10036041/runat_13012003_160808_7048/app_query.fasta_1.391
-DB-N_Geneseq_101002 -OFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXIT-0 -UNITS-bits -START-1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM-ext -HEARSIZE=500 -MINLEN-0 -MAXIEN=2000000000
-USER=US10036041_@CGN_1_1_79_@runat_13012003_160808_7048 -NCPU-6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPDP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq
Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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1852.815 Million cell updates/sec
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//SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*

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//SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*

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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AAS31128 ABQ54564 AAZ45606 AAT51048	1894 1396 1396 1396 1396	AAC9963 ABC9963 ABL34718 ABL34718 ABL12584 AAD12584 AAF94076 AAI99523 AAI99523 AAC64063 AAI95221 AAC02874 AAX39551 AAX39551 AAX39559 AAX39559 AAX39559	ABK35591 AAC64058 AAF93874 AAA96336 AAA95787 ABK35590 AAC99776 ABC99776 ABC99776 ABC99776
Human diagnostic a Human ovarian anti cDNA encoding poly Murine adipocyte c	Rat CDNA, SE Rat CDNA, SE Rat CDNA, SISOlated Human SBhACRP30a g Novel human gene. Human SBhACRP30a g Human SBhACRP30a g Human SBhACRP30B, Human genset metab Human novel polynu Murine ACRP30RIM c Mouse zacrp7 CDNA. CDNA encoding rat Skin cell cDNA, SE Rat CDNA, SE Rat CDNA, SE Rat CDNA isolated Human adipocyte co	cell cDNA, cell cDNA isolate cDNA isolate cDNA isolate cDNA isolate icDNA isolate icDNA isolate icDNA isolate icDNA isolate icDNA isolate icDNA encod n secreted place n secreted penceding no encoding no encodin	iption encoding no n zacrp3 cDM n zacrp3 cDM n cDNA encod encoding a n immune sys encoding no cell cDNA, cDNA isolate encoding ra encoding ra

ALIGNMENTS

RESULT 1 ABK35591 08-MAY-2002 (first entry) ABK35591; ABK35591 standard; DNA; 741 BP

Gene encoding novel human secreted or membrane-associated protein

Human; secreted protein; membrane-associated protein; hypertension; inflammatory disorder; neurological disorder; haematopoietic disorder; skeletal developmental disorder; growth abnormality; autoimmune disorder; neurodegenerative disorder; nervous system disorder; bacterial infection; peripheral myelinopathy; viral infection; cancer; obesity; diabetes; hypotension; sexual development disorder; blood disorder; gene; ds.

Homo sapiens

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Query Match:
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human secreted cor membrane-associated proteins and the genes encoding them. The sequences of the invention are useful for treating, preventing and the sequences of the invention are useful for treating, preventing and the sequences of the invention are useful for treating, preventing and the sequences of the invention of the blood cascade system including those leading to stroke, ABK35582-ABK35609 represent
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel secreted and membrane-associated polypeptides and polynucleotides encoding the polypeptides, for preventing, treating and ameliorating cancers, mental or sexual developmental disorders, and malignant tumours
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21-AUG-2000; 2000US-226517P.
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                                       ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu
                                                                                             LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly
                                                                                                                                                                                                     MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys
GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln
                          CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA
                                                                               AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCCTGGGCCACCGGGC
                                                                                                                                     CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT
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SMITHKLINE BEECHAM PLC.
GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                s encoding the novel human secreted of the invention
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Xiang Z, Xie
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Claim 31; Page 107-109; 123pp; English
                                                                                                                                                                                                     Homo
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                  infections, for wound healing energy efficiency in mammals
                                                                                    Piddington CS,
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                           Novel zacrp3 polypeptides used infections, for wound healing,
                                                                  WPI; 2000-665243/64.
                                                                                                                           20-APR-1999;
                                                                                                       (ZYMO ) ZYMOGENETICS INC.
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                                                                                    Bishop PD,
                                                                                                                                                                                                                                                                                SEQ ID NO:1.
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                           to treat or prevent bacterial or viral improving blood flow, and to analyze
                                                                                                                                                                                                                                  inhibition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the human zacrp3 protein (AAB29580) and to CC nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue cc of adipocyte complement related protein (ACRP30) and contains a CC collagen-ilke domain comprising Gly-xaa-Xaa or Gly-xaa-Pro repeats, and a CC cterminal Clq domain comprising 10 beta-strands. The zacrp3 gene is CC located on chromosome 5p12. The invention also relates to zacrp3 gene is CC located on chromosome containing zacrp3 polypeptides, calls cc zacrp3-specific antibodies, expression constructs and host cells CC comprising zacrp3 nucleic acids, and methods of recombinant production of CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the CC anorexia, and conditions associated with these disorders such as obesity and CC anorexia, and conditions associated with these disorders may be useful CC like domain, zacrp3 and zacrp3-containing fusion proteins may be useful CC as antimicrobial agents, promoting lysis or phagocytosis of infectious CC organisms such as bacteria or viruses. Zacrp3, its fragments, fusion CC contains, antibodies and activity modulators may also be used to inhibit collagen. Induced platelet aggregation, adhesion, or activation, and may therefore be treat injury to the vasculature or other collagence.
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This invention relates to nucleic acid sequences AAF93744 - AAF93916

CW which encode human secretory or membrane proteins represented by

CR AAB88317 - AAB88419. Included in the invention are primers

CR CAAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the

CR COMA sequences of the invention. The invention also includes methods for

CR the production of antibodies directed against the proteins, and cDNA

CR sequences, which can be used in vaccines. The polynucleotide sequences

CR can be used in gene therapy. The polynucleotide sequences and the

CR proteins they encode may be used in the prevention, treatment and

CR diagnosis of diseases associated with inappropriate secretory

CR protein/membrane protein expression. The nucleic acids and complementary

CR sequences may also be used as DNA probes in diagnostic assays

CR (e.g. polymerase chain reactions (PCR)) to detect and quantitate the

CR presence of similar nucleic acid sequences in samples. They may also be

CR used to study the expression and function of secretory proteins/membrane

CR polymeptides and their role in metabolism. The polypetides may be used

CR as antigens in the production of antibodies against them and in assays to

CR cl diagnosis to down regulate expression and activity. The antibodies may also be

CR agents to down regulate expression and activity. The antibodies may also
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                                                                                                                                                                                                                                                                                                                                        acids encoding secretory proteins/membrane proteins, useful
erapy or as candidate target molecules in drug development -
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                                                                                                                                                                                                                                                                                                              SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
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                                                     LeuLeuPheGluThrLys
                                                                                        ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe
                                                                                                                          SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu
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                                                                               CGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTC
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20-JUL-1999;
03-AUG-1999;
09-DEC-1999;
The present sequence encodes a secreted or transmembrane polypeptide. The specification describes polypeptides designated PRO1484, PRO4334, PRO1122, PRO1889, PRO1889, PRO1887, PRO1785, PRO4355, PRO4357, PRO4356, PRO4560, PRO4560, PRO4560, PRO4560, PRO4560, PRO5990, PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499, PRO1889 polypeptide is useful for diagnosing tumour in a mammal. The polypeptides, their agonists and antagonists are useful treating a condition associated with expression or activity of the polypeptide. Conditions treated include obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are capable of inducing proliferation of mammalian kidney mesangial cells and are therefore useful for treating kidney disorders associated with decreased mesangial cell function such as Bergers disease or other nephropathies associated with Schonlein-Henoch purpura, celiac disease,
                                                                                                                                                                                                                                                                                                                                                                                                                 Novel secreted and transmembrane polypeptides useful for diagnosing tumour in a mammal, for identifying agonists and antagonists of the polypeptide and for therapeutic use
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Stewart TA,
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99US-0146970.
99US-0170262.
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990S-0131291
990S-0132371
990S-0132379
990S-0132379
990S-0135750
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99US-0127035.
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Zhang Z;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1712 BP;
          AAA95787
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                                                                                                        ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe
                                                                                                                                                   SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu
                                                                                                                                                                                              TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys
                                                                                                                                                                                                                                         GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal
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                                                                                                                                                                                   TACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAA
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                                                                          LeuLeuPheGluThrLys
                                                                                                                                        TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTG
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Alignment Pred. No.:

Sequence 1760

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other;

Score:

Query

Match:

Percent Similarity: Best Local Similarity:

2.02e-99 1367.00 100.00% 100.00% 100.00% 21

Length:
Matches:
Conservative:
Mismatches:
Indels:

1760 246 0 0 0

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This sequence represents the cDNA for a human immune system molecule (C [IMOL] isolated as clone 1890540 from the Incyte BLAD70707 library. CC [Thoch human IMOLS (AAB15536-B1550)] and their encoding polynucleotides (AAA95775-A95789), and compositions comprising them are useful for the diagnosis, treatment or prevention of immunological disorders. The IMOL can be used to treat or prevent disorders associated with decreased (C e.g. inflammation, actinic keratosis, AIDS, Addison's disease), (C family for the development of antibodies that concers (e.g. actinic keratosis, arteriosclerosis, bursitis), and (C cancers (e.g. actinic keratosis, arteriosclerosis, bursitis), and (C cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also (C specifically recognizes these peptides. The polynucleotides may be used for the development of antibodies that (C expression of IMOL may be correlated with the disease, as targets in a microarray, to detect differences in gene sequences among normal, (C carrier and affected individuals, and for screening libraries of (C compounds in drug screening techniques. Antibodies which specifically be used for the disagnosis of disorders characterized (C bind to IMOL may be used for the disagnosis of disorders characterized (C with IMOL or agonists, antagonists, or inhibitors of IMOL.
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                                  Human; secreted protein; membrane-associated protein; hypertension; inflammatory disorder; neurological disorder; haematopoietic disord skeletal developmental disorder; growth abnormality; autoimmune disorder; eurodegenerative disorder; nervous system disorder; bacterial infeperipheral myelinopathy; viral infection; cancer; obesity; diabetes hypotension; sexual development disorder; blood disorder; gene; ds.
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cancer and ted polynucleotide used in the identification and encoding polypeptides used for treating i neurological diseases inflammatory of genetic

Claim 1; Page 317-318; 352pp; English.

The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and trabel inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.

Sequence 1035 BP; 255 A; 242 Ç 298 <u>ი</u> 240 ₽, 0

Match:

No.:

Length: Matches: Conservative: Mismatches:

Indels:

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US-10-036-041-2 (1-246) x AAC99776
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                                                                                                  HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe
                                                                                                                                                                                   GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal
                                                                                                                                       CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC
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                            GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG
                                                               GAGACCAACAT: TGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGGCCCCCCGTATCA
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                                                                                                            defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a cDNA of the invention.
                                                                                                                                                                                                                                                                   New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190357-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; rat; mouse; skin cell; skin wound; cancer; growth defect; developmental defect; inflammatory disease; dermatological; vulno immunomodulator; anti-inflammatory; cytostatic; neuroprotective;
                                                                                            Sequence
                                                                                                                                                                                       can be used
                                                                                                                                                                                                             The present invention provides the
                                                                                                                                                                                                                                                                                                                                             Watson
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                                                                                                                                                                       nt invention provides the protein and coding sequences of cDNAs from human, murine and rat skin cell libraries. The sequences ed in the development of therapputtic agents useful in the development of therapputtic agents useful in the of skin diseases, including skin wounds, cancer, growth
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                             Mouse zacrp2; adipocyte complement related protein homologue; ACRP30; C1q domain; collagen-like domain; energy balance modulat cellular metabolism; metabolic disorder; obesity; anorexia; antimicrobial agent; infection; platelet aggregation inhibition;
                                                               Mouse
                                                                                                     AAC64064
      Mus musculus
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                 zacrp3
                                                               zacrp2
                                                                                                     standard;
                         activation; vascular injury; antibacterial;
                                                               DNA,
                  homologue;
                                                                           (first entry)
                                                               SEQ
                                                                                                     DNA; 1117
                                                               ID NO:11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising zacrp3 nucleic acids, and methods of recombinant production of carpas. Human zacrp3, and its agonists and antagonists may be used in the study and modulation of cellular metabolism and energy balance in mammals, and may therefore be used to treat disorders such as obesity and anorexia, and conditions associated with these disorders. Due to its Clq like domain, zacrp3 and zacrp3-containing fusion proteins may be useful as antimicrobial agents, promoting lysis or phagocytosis of infectious organisms such as bacteria or viruses. Zacrp3, its fragments, fusion proteins, antibodies and activity modulators may also be used to inhibit collagen-induced platelet aggregation, adhesion, or activation, and may therefore have potential for promoting blood flow within the vasculature of a mammal e.g., to treat injury to the vasculature or other collagenous clisue. Human zacrp3 and its antibodies may additionally be used to study cdimerisation and oligomerisation. The present sequence represents DNA or consideration of the present sequence represents DNA or consideration and oligomerisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of adipocyte complement related protein (ACR930) and contains a collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and C-terminal Clq domain comprising 10 beta-strands. The zacrp3 gene is located on chromosome 5p12. The invention also relates to zacrp3 fragments, fusion proteins containing zacrp3 polypeptides, zacrp3-specific antibodies, expression constructs and host cells comprising zacrp3 replaced and morlein acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel zacrp3 polypeptides used to treat or prevent bacterial or viral infections, for wound healing, improving blood flow, and to analyze energy efficiency in mammals - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 115-117; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piddington CS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to the human zacrp3 protein (AAB29580) and leic acids which encode it (AAC64058, AAC64063). Zacrp3 is a h
                                                                                                                                                                                                                                            MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys
                                                                                                                                                 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly
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CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGGAACAATGGAGCTACTGGCCATGAA
                                                                      AAGTGTTGCCATGGAGATTATGGATTTCGTGGTTACCAAGGGCCCCCTGGACCTCCAGGT
                     ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu
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RESULT 10
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XX AAZ61
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AC AAZ61
XX Skin;
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                                                                                                                                                                                                                                                                embryonic skin cell; keratinocyte stem cell; transit amplifying cell
secreted; transmembrane; inflammation; cancer; neurological disease;
angiogenesis; tumour vascularisation; growth disorder;
developmental disorder; skin wound; hair follicle disorder;
                                                                                                                    29-APR-1998;
09-NOV-1998;
                                                                                                                                                                               04-NOV-1999
                                                                                                                                                                                                                                                      anti-inflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                        cDNA encoding rat skin cell secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ61633
                                                                                            (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                       29-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTA
                                                                                                                                                                                                                                                                                                                   dermal
                                                                                                                                                                                                                              sp
                                                                                                                                                                                                                                                                                                                                                                                                                  standard; cDNA; 1123
                                                                                                                                                                                                                                                                                                                  papilla; keratinocyte; neonatal
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                   98US-0069726
98US-0188930
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Novel polynucleotides useful for including wounds and cancer $\boldsymbol{\cdot}$

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Strachan L,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HTV-1 to leukocytes. The invention may also be used to treat growth and developmental effects, skin wounds and hair follicle disorders. Sequences AZS61506-Z61832 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences derived AZS6166-Z61649, AZS61725-Z61765, AZS61802-Z61811 and AZZ61826 encode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences AZS61650-Z61668, AZS61766-Z61780, AZS61812-Z61817 and AZS61827-Z61829 encode proteins with one or more putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1123 BP;
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                                                                             GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal
                                                                                                                         GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln
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                TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys
                                                                                                                                                                                                                                                         CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC
                                                                                                                                                                                                                                                                                         HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe
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TACCTTATGCACAATGGTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAA
                                                              GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG
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SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu

3.36e-95

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RESULT 11
AAZ61730
Alignment Scores: Pred. No.:
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                                                                                                                          dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences Az561006-z61802 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences Az56106-z61649, Az561725-z61765, Az561802-z61811 and Az561826 encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder;
                                                                                  proteins with an N-terminal signal sequence, indicating that the are secreted. Sequences AAZ61650-Z61668, AAZ61766-Z61780, AAZ618 and AAZ61827-Z61829 encode proteins with one or more putative
                                         Sequence
                                                                                                                                                                                                                                                                                                           The invention relates
                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 137; 235pp; English.
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09-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                    polynucleotides useful ding wounds and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                  AAY76025
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                                         BP;
                                                                      domains.
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98US-0188930,
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                                         277 A;
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                                                                                                                                                                                                                                                                                                         to novel nucleic acid sequences derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246
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AAZ61812-Z61817
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Best Local
Query Match
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Rat; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnerary; immunomodulatory; keratinocyte growth stimulation; cancer; angiogenesis in
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Best Local Similarity:
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mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immundeficiency virus (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns
                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide used in the identification disorders and encoding polypeptides used for treating
                                                                                                                                                                                                                                                                                           Claim 1; Page 87; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation; neurological
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)B; AAB55908.
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Length:
Matches:
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                                                                         The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of
tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukcytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in
                                                                                                                                                                                                                                    Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                             Seguence 1123
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al defect; inflammatory disease; dermatological; vulnerary;
ator; anti-inflammatory; cytostatic; neuroprotective; gene;
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2000US-221232P
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Claim 1; Page 155-156; 466pp;

English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a cDNA of the invention.
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GlyValTyrPhePheThrPheSerMetLysHisGluAspValGluGluValTyrVal
                                                                                                                                                                                                                                           GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
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Search completed: January 15, 2003, 19:51:11 Job time: 304 secs

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Command line parameters:

MODEL=frame+_p2n.model -DEV=xlp
-Q-/Cgn21/USPTO_Spool/US10036041/runat_13012003_160809_7088/app_query.fasta_1.391
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST-45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER-US10036041 @CGN 1_1_31 @runat_13012003_160809_7088 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                   US-09-188-930-28

US-09-188-930-203

US-09-188-930-217

US-08-463-911-1

US-08-463-911-6

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203, App
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ALIGNMENTS

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US-10-036-041-2 (1-246) x US-09-188-930-28 (1-1123)
                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                       Score
                                                                                                                        Pred. No.:
                                                                                                                                      Alignment Scores:
                                                                                                                                                                           ; ORGANISM: Rat
US-09-188-930-28
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US-09-188-930-28
                                                 Query
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                            TYPE: DNA
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                                               1.21e-117
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Matches:
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RESULT 2
US-09-188-930-203
                    NUMBER OF SEQ ID NOS: 348
SOFTWARE: FRANCSEQ FOR WINDOWS VERSION
SEQ ID NO 203
LENGTH: 1123
TYPE: DNA
CORGANIZM: Rat
US-09-188-930-203
                                                                                                       APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: OF LORNA
APPLICANT: Murison, Matthew
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
APPLICATON: Compositions Isolated From S
TITLE OF INVENTION: and Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
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GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Is
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CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
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                                                                                        LysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPhe
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CGCATTCGGACTTTTGACGCCAACACCGGCCAACCACGACGTGGCCTCGGGCTCCACCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI95-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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42 CysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGlyPro
                                                                24 AspGluTyrMetGluSerProGlnThrGlyGly-----LeuProProAspCysSerLys
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                                                                                                                              4 ArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCysLeuCysGln
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                                  GATGACGTTACTACAACTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCAAGGGAACT 159
                                                                                                  AGGATGCTACTGTTGCAAGCTCTCCTGTTCCTCTTAATCCTGCCC---AGTCATGCCGAA
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Matches:
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Length:
Matches:
Conservative: Mismatches: Indels:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08463911 Patent No. 5869330 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
ATTORNEY/AGENT INFORMATION:
NAME: GIADADAN, PATTICLA
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                           COUNTRY:
ZIP: 021
                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                            FILING DATE:
CLASSIFICATION:
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                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                               ITY: Lexington
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WENTION: A NOVEL SERUM PROTEIN PRODUCED
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; LOCATION:
US-08-463-911-6
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 bass ---
TYPP
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 --- CCTGCACAGGCTGGATG-GCGGGCATCCCAGGGCATCCGGGCCATAATGGGGCCCCA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 --- CCGGAGTCCTGCTTCCCCTGCCCAAGGGGG---
                                                                                                                                                  179 TyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                           352 TTTCCGGGAATCCAAGGCAGAAAGGAGAACCTGGAGAAGGTGCCTATGTATACCGCTCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 TyrProGlyIle----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 LeuGlyProArg------GlyGluArgGlyGlnHisGlyProLysGlyGluLysGly 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 GlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGlyAspLysGlyAsp-------
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TrpLeuArgMet---GlyAsnGly-----
                                      AATAATGTGGACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTC
                                                                      GlyLysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluVal
                                                                                                                AAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAA
                                                                                                                                                                                          ATTCCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTAT-----ATGAAGGATGTG
                                                                                                                                                                                                                            ValSerGlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluVal 178
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APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
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SEQ ID NO 9
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR US
FILE REFERENCE: 210121.475C1
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TYPE: DNA
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                                                             GGAGACTCCCGTAGCATGACCCCTGTGGATGTGCCAGTGACAAATCCAGCAGCCACCATA
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ARLIER FILING DATE: 1997-07-08
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Alignment Scores:
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 Percent Similarity:
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SEQ ID NO 51
LENGTH: 1333
                                                                            FEATURE:
NAME/KEY: SITE
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GENERAL INFORMATION:
APPLICANT: Sheppard, Paul
APPLICANT: Humes, Jacqueli
                                               Sequence 1, Application Patent No. 6197930
                                                                                 -09-140-804-1
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS FILE REFERENCE: 97-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version
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TYPE: DNA
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LOCATION: (198)...
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PheAlaGlyPheLeuLeuPhe 243
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                                                 LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGly-----
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                                                                                                                    AAGCCAGCCTCGCTCTCGGGGGGGGGCCATGGTGAGGCCTGGAGGACCAAGTGTGG
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                                                                                LeuArgMetGlyAsnGly------AlaLeuHisGlyAspHisGlnArgPheSerThr 236
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TTCTCCGGATTTCTGGTGTAC 896

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GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: MCKAY, C.
APPLICANT: MCKAY, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND US
TITLE OF INVENTION: SECRETED PROTEINS AND US
FILE REFERENCE: 7853-144
CCURRENT APPLICATION NUMBER: US/09/336,536
CCURRENT APPLICATION NUMBER: US/09/336,536
CCURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
SEQ ID NO 9
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                                  CTTGTCAAAAACGGGCAGTCCATCGCCTCTTTCTTCCAGTAT---TTTGGGGGGGTGGCCC
                                                                  LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGly-----
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CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
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Patent No. 6406884
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APPLICANT: McRay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND
FILE REFERENCE: 7853-144
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TYPE: DNA
ORGANISM: Mus musculus
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                 GlyAspLeuGlyProArgGlyGlu------ArgGlyGlnHisGlyProLysGlyGlu 106
                                                                                                                                                                                                                                                                  AsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGlyAspLys
                                                            GAGAGCCGGGTACCTCCGCCAGCCGACACACCCCTACCTTTCGACCGTGTGCTGCTAAAT
                                                                                         LeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsn 143
                                                                                                                        ATCGGGCCTGCGGGGGGGGTGCTCGGTACCCCCACGATCAGCCTTCAGTGCCAAGCGATCC
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GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew

APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
ITILE OF INVENTION: Compositions Isolated From Skin Cells
ITILE OF INVENTION: and Methods For Their Use
ITILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348
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US-09-188-930-30
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NAME/KEY: unsure

LOCATION: (545)...(545)

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SEQ ID NO 30
LENGTH: 1015
TYPE: DNA
ORGANISM: Rat
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813 TTCTCTGGATTTCTCGTCTAT 833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                693 AAGCCAGCCTCGCTCTCAGGGGGTGCGATGGTAAGGCTAGAACCTGAGGACCAGGTGTGG
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                                                                                                    359 GACGGCCGTGATCGCCGGACGCTGCACCCCGGAGCTCCGGGAGAGAAAGGCGAGGCGGG 418
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                                                      68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGly 87
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                                                                                                                                                                                                        GlnThrGlyGlyLeuProProAspCysSerLys------CysCysHisGlyAspTyr 47
                                                                                                                                     SerPheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsn 67
AspLysGlyAspLeuGlyProArgGlyGlu----
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18.62%
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Indels:
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Conservative:
 --ArgGlyGlnHisGlyProLys 104
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Oy 31 GlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyr 47	
Qy 11 LeuLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGluSerPro 30	
US-10-036-041-2 (1-246) x US-09-188-930-218 (1-1001)	
Alignment Scores: 1.31e-15 Length: 1001 Score: 252.50 Matches: 79 Percent Similarity: 45.788 Conservative: 35 Best Local Similarity: 31.738 Mismatches: 100 Query Match: 38.478 Indels: 35 DB: Gaps: 10	
RESULT 13 US-09-188-930-218 Sequence 218, Application US/09188930A ; Sequence 218, Application US/09188930A ; Patent No. 6150502 ; Pate	
Qy 235 SerThrPheAlaGlyPheLeuLeuPhe 243 ::: ::::: Db 884 AGTACCTTCTCGGATTTCTCGTCTAT 910	
Qy 218 ValTrpLeuArgMetGlyAsnGlyAlaLeuH1SGlYASPH1SGINAF9FHE 234 ::::::::::::::::::::::::::::::	н о
ASPThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGlu 21:	
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Oy 142 ThrasnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSerGly 161	מ ש
Oy 122 AlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerValGlu 141	U 0
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APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND US:
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 728
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US-09-336-536-2
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 Query Match:
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                                                                                                                                                                                                                                                                                          APPLICANT: Leiby, K. APPLICANT: McKay, C.
                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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; TYPE: DNA
; ORGANISM: HOMO
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                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TILLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 783-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEC ID NOS: 75
COUNTIESE DEFORMATIONS: 75
                                                                                                                                                                                 SEQ ID NO 1
LENGTH: 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09336536 Patent No. 6406884
                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
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                                                                    745 AAGCCAGCCTCGCGCGCGGGGGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGG 804
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                                                                                                      220 LeuArgMetGlyAsnGly------AlaLeuHisGlyAspHisGlnArgPheSerThr 236
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                  PheAlaGlyPheLeuLeuPhe 243
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Matches:
Conservative:
Mismatches:
Indels:
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Search completed: January 15, 2003, 21:21:52 Job time: 77 secs

GenCore version 5.1.3 Compugen Ltd.

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Command line parameters:

MODEL-frame+_p2n.model -DEV=xlp
-MODEL-frame+_p2n.model -DEV=xlp
-Q-/cgn2_1/USPTO_Spool_VS10036041/runat_13012003_160808_7058/app_guery.fasta_1.391
-QB-GenEmbl -QFMT-fastap -SUFFIX-p2n.rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATFIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_M1N-0 -ALIGN-15 -MODE-LOCAL
-QUERT-200 -THR_SCORE-pct -THR_MAX-100 -THR_M1N-0 -ALIGN-15 -MODE-LOCAL
-QUERT-200 -THR_SCORE-pct -THR_MAX-100 -MAXLEN-200000000
-USER-US10036041_@CGN_1_1_337_@TUNATL_3012003_160808_7058 -NCPU=6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NGE_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARR_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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             GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer
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ZymoGenetics, Inc. (US)
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                                                                Direct Submission
Submitted (200-DEC-2000) Bioinformatics,
Submitted Ave. East, Seattle, WA 98102,
Location/Qualifiers
                                                                                                                                                                                                                                                   Homo sapiens complement-c1q tumor necrosis (CTRP3) mRNA, complete cds.
                                                                                                         2 (bases 1 to 1710) Piddington, C.S. and Direct Submission
                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1710)
Piddington,C.S. and Bishop,P.
                                                                                                                                                     Homo sapiens complement-clq
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                                                                                                                                                                                                                                          AF329837.1
                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
           /map="5p13-p12"
1. .1710
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                                                                                                                      and Bishop, P
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Primates;
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/protein_id="AAK17961.1"
/db_xref="GI:13374520"
/trans!ation="MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCH
/trans!ation="MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCH
GDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERQOHG
PKGEKGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVS
GYYFFTFSMKKHEDVEEVYYYLMHNGRTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-DEC-2000) Department of Radiology and Radiation Oncology, Graduate School of Dentistry, Osaka University, 1-8 Yamadaoka, Suita, Osaka 565-0871, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the human CORS26 gene Unpublished
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GDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHG
PKGEKGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative secretory protein CORS26"
/protein_id="AAK70344.1"
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Sequence 11 from
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Piddington, C.S. and Bishop, P.D.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                 /protein_id="CAC16633.1"
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//db_xref="G1:11229977"
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Mus musculus
Eukaryota; Metazoa; Chordata; C.
Manmalia; Eutheria; Rodentia; S.
1 (bases 1 to 1879)
Maeda,T., Abe,M., Kurisu,K., Ji)
Molecular cloning and character
                                                                           1879 bp mRNA
Mus musculus collagenous repeat-containing
protein (CORS26) mRNA, complete cds.
AF246265
AF246265.1 GI:11275676
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Indels:
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                               LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding a putative secretory protein and in skeletal development J. Biol. Chem. 276 (5), 3628-3634 (2001) 21264842
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GVYFFTFSMMKHEDVEEVYVYLMHGGNTVFSMYSYETKGKSDTSSNHAVLKLAKGDEV
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Kato,S. and Kimura,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AX191537
Sequence 59
AX191537
AX191537.1
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Protegene Inc. (JP) ; SAGAMI CHEMICAL
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Secretory protein or membrane protein Patent: EP 1067182-A 510 10-JAN-2001;
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QY 68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGly	48 S 361 A	Db 301 CAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTAC	Qy 29SerProGlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyr	Db 241 CCAGATGAGCTACCGCACCCCGAGGTAGATGACCTAGCCCAGATCACCACATTCTGGGGC	Qy 28	Db 181 AGCCATCCTAAAACTGGGACTGTGGATAATAACACTTCTACAGACCTAAAATCCCTGAGA	Оу 28	Db 121 GTGCAAAGCCACCAGCAGACTGGCCGTAGCGGCTCCAGGAGGGAAAGTGAGAGAGGGG	Qy 28	Qy 21 LeuCysGlnAspGluTyrMetGlu	Qy 1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys	US-10-036-041-2 (1-246) x AX191527 (1-672)	Mismatches: Indels: Gaps:	Alignment Scores: Pred. No.: 1.38e-52 Length: Score: 792.50 Matches: 150 Percent Similarity: 66.96% Conservative: 0		/organism="Homo sapiens" /db_xref="taxon:9606" BASE COUNT 185 a 170 c 187 g 130 t	ocation/Qualifiers	JOURNAL PATENT: WO 0149728-A 49 12-JUL-2001; Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)	Kat		SOURCE human ORGANISM Homo sapiens	. 2	LOCUS AX191527 672 bp DNA linear PAT 15- DEFINITION Sequence 49 from Patent WOO149728. ACCESSION AX191527	RESULT 10 AX191527	Db 721 YTNYTNTTYGARACNAAR 738	Qy 241 LeuLeuPheGluThrLys 246	Db 661 MGNATGGGNAAYGGNGCNYTNCAYGGNGAYCAYCARMGNTTYWSNACNTTYGCNGGNTTY	Qy 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe	Db 601 WSNGAYACNWSNAAYCAYGCNGTNYTNAARYTNGCNAARGGNGAYGARGTNTGGYTN 660
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Hel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Cteman and Anuradha Madan
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 546)
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Baker, K. P., Goddard, A. and Wood, W. I.
Human polypeptides and methods for the use thereof
Patent: WO 0107611-A 240 01-FEB-2001;
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Submitted (20-DEC-2000) Bioinformatics, ZymoGenetics, Inc.,
Eastlake Ave. East, Seattle, WA 98102, USA
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Piddington, C.S., Sheppard, P.O.,
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/translation="MrVLLYVTSFAICASGQDRGNQLKGENYSPRYICSIPGLPGPPG

PPGANGSPGPHGRIGLPGRDGRDGRKGEKGEKGTAGLRGKTGPLGLAGEKGDQGETGK

KGPIGPEGEKGEVGPIGPPGPKGDRGEGGDPGLPGVCRCGSIVKSAFSVGITTSYPE

ERLPIIFNKYLFNEGEHYNDATGKFCAPPGTYYFSVDITLANKHLAIGUVHNGOYRI

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                                Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue procurement: miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Sh
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC022187 3959 bp mRNA linear PRI 28-
Homo sapiens, complement-clq tumor necrosis factor-related
7, clone MGC:26871 IMAGE:4825040, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Clone
                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC022187.1
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  distribution:
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  MGC
  clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
  distribution information
                                           and Michelle Whiting
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Best Local Similarity:
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  GlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspVal
                                              TGTGGAAGCATCGTGCTCAAATCCGCCTTTTCTGTTGGCATCACAACCAGCTACCCAGAA
                                                                                                                                   CCTGGACCAAAGGGAGACAGAGGAGAACAAGGGGACCCGGGGCTGCCTGGAGTTTGCAGA
                                                                                                                                                                                                                      GGGAAGAAAGGACCCATAGGACCAGAGGGAGAGAAAGGAGAAGTAGGTCCAATTGGTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL Series: IRAK Plate: 33 ROW: k Column: 8
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PPGANGSPGPHGRIGLPGRDGRDGRKGEKGEKGTAGLRGKTGPLGLAGEKGDQGETGK
KGPIGPEGEKGEVGPIGPPGPKGDRGEQGDPGLPGVCRCGSIVLKSAFSVGITTSYPE
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/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
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KTFDANTGNHDVASGSTVIYLQPEDEVWLEIFFTDQNGLFSDPGWADSLFSGFLLYVD
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/db_xref="GI:18381163"
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/db_xref="taxon:9606"
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Search completed: January 15, 2003, 20:42:58 Job time : 3099 $\sec s$

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Command line parameters:

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-MODEL-frame+p2n.model 'DEV-xlp
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-OP/cgn2_1/USPTO_Spool_VS110036041/runat_13012003_160809_7069/app_query.fasta_1.391
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-UNITS-bits 'START-1 'END-1 'MATRIX-B-blosum62 'TRANS-human40.cdi 'LIST-45
-DOCALIGN-200 'THR_SCORE-pct 'THR_MAX-100 'THR_MIX-0 'ALIGN-15 'NODE-LOCAL
-OUTFMT-P10 'NORM-ext 'HEAPSIZE-500 'MINLEN-0 'MAXLEN-200000000
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-USER-US10036041_CGN_11_11716_0*UNATL_13012003_160809_7069 'NCPU-6 'ICPU-3
-UNATRI_TIMEOUT-30 'THREADS-1 'XGAPOP-10 'XGAPEXT-0.5 'FGAPOP-6 'FGAPEXT-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	19 20 20 22 22 23 24 24 25 26 27 27 33 33	c 1171111111111111111111111111111111111	Result No.
629 629 620 568 546 513 453.5 429.5 411 411	733 721 721 715 689 667 667 668 668 668 633 633	1238.5 1137.5 11093 11055 10055 995.5 995.5 9958 9958 9958 9758 9764.5	1.0
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ALIGNMENTS

AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BM924169	RESULT 1
NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	<pre>Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1103)</pre>	Homo sapiens	human.	EST.	BM924169.1 GI:19374548	BM924169	5', mRNA sequence.	AGENCOURT_6630525 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760396	BM924169 1103 bp mRNA linear EST 12-MAR-2002		

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GluThrAsnI1eGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer
                                                HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
                                                                                                                                                                                      ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
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Tissue Procurement: Life Technologies,
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Contact: Robert St
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Plate: LLAM12807 row
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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/lab_host="DH10B"
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Tissue Procurement: Life Technologies,
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                              /note-*Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-df primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb, Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library.*
                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:5199982"
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/db_xref="taxon:9606"
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           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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           GlyValTyrPhePheThrPheSerMetMetLysHisGluAspVal-GluGluValTyrVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA.Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa. Site_2: NotI; Cloned unidirectionally. Primer: Oligo Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

a 236 c 280 g 231 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_bost="DH10B"
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/strain="FVB/N-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1956432 724 bp mRNA ul77b06;yl Sugano mouse kidney mkia Mus IMAGE:2136563 5' similar to SW:CERL_RAT GLYCOPROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 724)
                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free
TMAGE Consortium (info@image.llnl.gov
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                                                      primer CGACCTGCAGCTCGAGCACA.
           Institute of Medical Science). Custom primers sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG
                                constructed by Dr. Sumio Sugano (University of Tokyo
                                            performed to exclude fragments <1.5kb.
                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:2136563"
                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL"
                                                                                                                                          /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
                                                                                                                                                     /lab_host="DH10B"
                                                                                                                                                                               /sex="
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Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Expressed sequence tag analysis of human retina
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hd17a10.yl Human Retina
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MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
                                                                                                                           GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGGCCTCGAGGGGAGCGGGGGCAG
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                                          CATGGCCCCAAAGGAGAGAGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC
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Contact: Wistow G
Section on Molecular Structure and Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: graeme@helix.nih.gov
Plate: 17 row: a Column: 10
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Tel: 301 402 3452
Fax: 301 496 0078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Eye; Vector: pSPORT1; Neural retina.tissue /note="Organ: Eye; Vector: pSPORT1; Neural retina.tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the psport vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGACCGCCCCT]15-3']. EST analysis was performed on the unamplified library at the NIH Intranural Sequencing Center (NISC)."
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/db_xref="taxon:9606"
/clone="hd17a10"
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/dev_stage="Adult"
/lab_host="EMDH10B"
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AI006567

BY BURNA Linear EST 12-JUN-
Uel4d08.yl Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:1480335 5' similar to SW:CERL_RAT P98087 CEREBELLIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity Seg primer: primer name ambiguous High quality sequence stop: 471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 692)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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314 286 1810
                                       /note="vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
/note="vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAAGCTGCG and 3' end primer
CGACTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1480335"
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                   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                       AI527737
680 bp ruj28e09.yl Sugano mouse kidney mkia
IMAGE:1921288 5', mRNA sequence.
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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This clone is available royalty-free
IMAGE Consortium (info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, Tel: 314 286 1800 Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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/Clone_lib="NCI_CGAP_Kid14"
/Clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer: Oli
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
154 c 176 g 120 t
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9850 row: g column: 02
High quality sequence stop: 629.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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National Institutes of Health, Mammalian
Unpublished (1999)
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BF784596.1 GI:120
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                                                                   un02e01.y1 Sugano mouse kidney mkia Mus IMAGE:2372664 5' similar to SW:CERL_RAT GLYCOPROTEIN. ;, mRNA sequence.
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/clone_lib="NCI_CAP_Kid14"
/clone_lib="NCI_CAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1:
Site_2: SalI; Cloned unidirectionally. Primer: Oli
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,M., Schurk,R., Ritte; E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1012316
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Fax: 314 286 1810
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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77 a 172 c 156 g 146 t 5 others
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/clone="IMAGE:2372664"
/clone_lib="Sugano mouse
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1 (bases 1 to 635)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Sasaki, M., Koya, S., Matsuyama, T., Sakai, C., Sakai, K., Sano, H., Sasaki, Okazaki, Y., Okida, T., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., D., Shibata, K., Shinagawa, A., Shiraki, T., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                        Email: genome resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Nov 30, 2000 this sequence version replaced gi:11468663.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Debay Contacts (2002)
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                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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  encyclopedia: real-time sequence clustering
                                              Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,,Y. and Hayashizaki,Y.
                           Computer-based methods for the mouse full-length cDNA
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Best Local Similarity:
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                                                                       ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
                                                                                                                                                                              LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly
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Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Project of Genome Exploration Research Group in Rik
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/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: Sal1; Site_2: BamH1; cDNA library was
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/clone_lib="RIKEN full-length enriched,
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2010)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                            encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KOndo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-7-22 Suehiro-cho, Tsurumi-ku, Tel: 81-45-503-9222
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                      Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                         Computational Analysis of Full-Length Mouse cDNAs Compared with luman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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cDNA clone C130060D14 5', mRNA sequence
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                                            GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer
                                                                                             ATGGCTTCTCTAGCAACTCACTTCAGCAATCAGAACAGGGGCATTATCTTCAGCAGTGTT
                                                                                                                 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal
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GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
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/lab_host="DH10B"
/note="Site_1: SalI; Site_2:
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/clone="C130060D14"
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/strain="C57BL/6J"
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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genes. Genome Res. 10 (10), 1617-1630 (2000)
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
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Contact: Yoshihide Hayashizaki
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahar
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Computer-based methods for the mouse full-length cDNA
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AI316916 571 bp uj24c04.y1 Sugano mouse kidney
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US-10-036-041-2 (1-246) x BB610546 (1-662)
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                                                                                                                                                                                                                                                                                                                                                                  TyrLeuMet 183
                                                                                                                                    GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
                                                                                                                                                                                                        GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
                                                                                                                                                                                                                                                                                                 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
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                                                                          GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGGGGAGATTTGGGGGCCCCCTA-TCA
                                                                                                                                                                                                                                                                              ATGGCTTCTCTAGCAACTCACTTTAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT
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TTCCCTATG
647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site_1: XhoI; Site_2: SstI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="SOLR"
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p mRNA linear EST 17-mkia Mus musculus cDNA clone

EST 17-DEC-1998

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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMAGE:1920870 5', mRNA sequence.
AI316916
AI316916.1 GI:4032183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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154 c 156 g 118 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constructed by Dr. Sumio Sugano (University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Sugano mouse kidney mkia"
/sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 828)
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602464652F1 NIH_MGC_75 Homo sapiens
                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1331 row: h column: 14
High quality sequence stop: 740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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/clone="IMAGE:4592701"
/clone=lib="NIH_MGC_75"
/clone=lib="NIH_MGC_75"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); S' and
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc); S' and
3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTACAGGCCGAGCGGCGACATG-dT[30]BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4, 0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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s cDNA clone IMAGE:4592701
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149
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                                         362
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Search completed: January 15, 2003, 21:20:27 Job time : 2243 secs

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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgp2_1/USPTQ_Spool/US10036041/runat_13012003_160809_7112/app_query.fasta_1.391
-Q-/cgp2_1/USPTQ_Spool/US10036041/runat_13012003_160809_7112/app_query.fasta_1.391
-DB-Published_Applications_NA -QFMT-fastap -SUFFIX-p2n.rnpb -MINMATCH-0.1
-LOOPEXT-0 -UONITS-bits -START-1 -END--1 -MATRIX-blosum62
-TRANS-Pumman40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US10036041 @CGN _11_36_@runat_13012003_160809_7112
-NCPU-5 - ICPU-3 - NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS=1 -XGAPOF=10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Maximum DB seq length: 200000000
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s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                    No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed,
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ALIGNMENTS

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US-10-036-041-1
Sequence 1, Application US/10036041
Publication No. US20020192751A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Caton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCIDS ENCODING THE SAME
FILE REFERENCE: P3030R1C8
CURRENT APPLICATION NUMBER: US/10/036,041
CURRENT APPLICATION NUMBER: 60/112514
PRIOR APPLICATION NUMBER: 60/112514
PRIOR APPLICATION NUMBER: 60/112514
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-12
PRIOR APPLICATION NUMBER: 60/113430
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
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LENGTH: 1712
TYPE: DNA
ORGANISM: Homo
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PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DAYE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: PCT/US01/19692
FILING DATE: 2001-06-20
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APPLICATION NUMBER: PCT/US00/34956
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APPLICATION NUMBER: PCT/US00/32678
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                                          GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGGCCCCAGTATCA
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Matches:
Conservative:
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Indels:
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FILING DATE: 1999-04-27
APPLICATION NUMBER: 60/131272
FILING DATE: 1999-04-27
APPLICATION NUMBER: 60/131291

APPLICATION NUMBER: 60/131270 FILING DATE: 1999-04-27 APPLICATION NUMBER: 60/130359 FILING DATE: 1999-04-21 FILING DATE: 1999-04-1 APPLICATION NUMBER: 60/129122 APPLICATION NUMBER: 60/127706 FILING DATE: 1999-04-05

FILING DATE:

1999-03-31

FILING DATE: 1999-03-24
APPLICATION NUMBER: 60/127035

APPLICATION NUMBER: 60/125826

1999-03-23

FILING DATE:

FILING DATE: 1999-03-23 APPLICATION NUMBER: 60/125778

APPLICATION NUMBER: 60/125774

APPLICATION NUMBER: 60/115552 FILING DATE: 1999-01-12 APPLICATION NUMBER: 60/116843 FILING DATE: 1999-01-22

APPLICATION NUMBER: 60/114140 FILING DATE: 1998-12-23

APPLICATION NUMBER: 60/113621 APPLICATION NUMBER: 60/113605 FILING DATE: 1998-12-23

1998-12-

OR APPLICATION NUMBER: 09/747259
OR FILING DATE: 2000-12-20
OR APPLICATION NUMBER: 09/816744
OR FILING DATE: 2001-03-22
OR APPLICATION NUMBER: 09/854208
OR FILING DATE: 2001-05-10
OR APPLICATION NUMBER: 09/854280
OR FILING DATE: 2001-05-10
OR APPLICATION NUMBER: 09/874503
OR FILING DATE: 2001-06-05

APPLICATION NUMBER: 09/644848 FILING DATE: 2000-08-22

FILING DATE:

FILING DATE:

APPLICATION NUMBER: 09/380142 FILING DATE: 1999-10-29
APPLICATION NUMBER: 09/311832

1999-08-25 1999-05-14 APPLICATION NUMBER: 60/138166 FILING DATE: 1999-06-08 APPLICATION NUMBER: 60/144791 FILING DATE: 1999-07-20

APPLICATION NUMBER: 60/146970 FILING DATE: 1999-08-03

APPLICATION NUMBER: 60/162506

FILING DATE: 1999-05-04
APPLICATION NUMBER: 60/135750
FILING DATE: 1999-05-25

APPLICATION NUMBER:

60/132383

APPLICATION NUMBER: 60/132379 FILING DATE: 1999-05-04

APPLICATION NUMBER: 60/132371

LING DATE: 1999-05-04

APPLICATION NUMBER: 09/908,827
FILING DATE: 2001-07-18
APPLICATION NUMBER: PCT/US99/10733
FILING DATE: 1999-05-14
APPLICATION NUMBER: PCT/US99/28551
FILING DATE: 1999-12-02

APPLICATION NUMBER: PCT/US99/30720

APPLICATION NUMBER: 09/ FILING DATE: 2001-06-29

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PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-12-15
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PRIOR FILING DATE: 1998-12-25
PRIOR PELLING DATE: 1998-12-22
PRIOR PELLING DATE: 1998-12-23
PRIOR PELLING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/11552
PRIOR APPLICATION NUMBER: 60/116843
PRIOR PELLING DATE: 1999-01-12
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APPLICANT:
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APPLICANT: Zhang, Zemin Price Polypeptides and NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3030R1C4
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FILING DATE: 1999-03-24
APPLICATION NUMBER: 60/
FILING DATE: 1999-03-31
APPLICATION NUMBER: 60/129122
FILING DATE: 1999-04-13
APPLICATION NUMBER: 60/130359
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Gurney, Austin L.
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OR APPLICATION NUMBER: 09/816744
OR FILING DATE: 2001-05-10
OR APPLICATION NUMBER: 09/854208
OR FILING DATE: 2001-05-10
OR APPLICATION NUMBER: 09/854280
OR FILING DATE: 2001-05-10
OR APPLICATION NUMBER: 09/85959
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OR APPLICATION NUMBER: PCT/US00/05601
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OR APPLICATION NUMBER: PCT/US99/28551
OR FILING DATE: 1999-12-02
OR APPLICATION NUMBER: PCT/US99/30720
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DR APPLICATION NUMBER: PCT/US00/34956

DR FILING DATE: 2000-12-20

DR APPLICATION NUMBER: PCT/US01/06520

DR FILING DATE: 2001-02-28

DR APPLICATION NUMBER: PCT/US01/17800

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FILING DATE: 1999-05-14
APPLICATION NUMBER: 09/380142
FILING DATE: 1999-08-25
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; ORGANISM: Homo Sapien
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PRIOR APPLICATION NUMBER: 60/112514
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PRIOR APPLICATION NUMBER: 60/125774
PRIOR FILING DATE: 1999-03-23
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APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul
APPLICANT: Gurney, Austin
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                                                                                                                                                                                                                                                                                                              LENGTH: 1712
TYPE: DNA
ORGANISM: HOMO
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PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
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APPLICATION NUMBER: PCT/US99/10733
FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/869599
FILING DATE: 2001-06-29
APPLICATION NUMBER: 09/908,827
FILING DATE: 2001-07-18
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APPLICATION NUMBER: 09/854208
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APPLICATION NUMBER: 09/747259
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APPLICATION NUMBER: PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
                                                 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 359
LENGTH: 1608
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-849A-359
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                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                        Patent No.
                                                                                                                      APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
                                                               PRIOR APPLICATION NUMBER: 60/195,582 PRIOR FILING DATE: 2000-04-06 NUMBER OF SEQ ID NOS: 598
                                                                                                 CURRENT APPLICATION NUMBER: US/09/822,849A CURRENT FILING DATE: 2001-09-04
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                                                                                                                                                                                                                                               INFORMATION
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                                                                                                                                                                                                                         Clark,
                                                                                                                                                     Howes, Steven H.
Resnick, Richard J.
Gulukota, Kamalakar
Graham, James R.
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APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Vamazaki, Vicki
APPLICANT: Ujwal, Manusha L.
APPLICANT: Ujwal, Manusha L.
APPLICANT: Unmanac, Radoje T.
TITLE OF INVENTION: NO. US20020111302A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 799
CURRENT APPLICATION NUMBER: US/09/728,952
CURRENT FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Pt_FL_genes Version 2.0
SEQ ID NO 85
LENGTH: 1297
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (80)..(949)
US-09-728-952-85
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; Sequence 85, Application US/09728952
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PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
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APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
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ORGANISM: mus musculus
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GACGGCAGCACTGGCAAGTTCTACTGCAACATTCCGGGACTCTACTACTACTTCTCTTACCAC 543
                     SerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePhe 148
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Best Local Similarity:
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PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
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APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10
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SOFTWARE: Patent.pm
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TYPE: DNA
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RAIALYSG1YG1uLySG1YASpLYSG1YASpLeuG1YProArgG1YG1uArg-------98
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US-10-036-041-2 (1-246) x US-09-909-547-3 (1-1276)
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LENGTH: 1276
TYPE: DNA
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APPLICANT: Yen, I
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PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
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CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/776,976
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            CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/199,881
PRIOR APPLICATION NUMBER: US 60/299,881
                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09776976 Patent No. US20020037849A1 GENERAL INFORMATION:
                                                                                                                                                                                                                      APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and
                                                                                                                                                                                                 FILE REFERENCE: 76.US4.REG
                                                                                                                                                                                                                                                                                  APPLICANT: Fruebis, Joachim APPLICANT: Erickson, Mary
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Percent Similarity:
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CURRENT FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR APPLICATION NUMBER: US 60/299,881
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TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
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SOFTWARE: Patent.pm
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                                                                                                                                      GlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMetLysHis 172
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                                                GluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMet 192
                                                                                                          GGTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTAT
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APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                    GlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLySGlyGluLySGlyAsp 88
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PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: Patentin version 3.0
SEQ ID NO 235
LENGTH: 4517
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PRIOR EILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
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TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Sets
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Gaps:
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29 SerProGlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyrSer 48

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APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Us:
FILE REFERENCE: 76.US4.REG
CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR TILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
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US-09-776-976-1
                                   NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09776976 Patent No. US20020037849A1 GENERAL INFORMATION: APPLICANT: Fruebis, Joachim
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APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Fruebis,
APPLICANT: Erickso
APPLICANT: Yen, Fr
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RESULT 14
US-09-758-055-1
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Sequence 1, Application US/09758055 Patent No. US20020058617A1
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Fruebis, Joachim Yen, Frances Erickson, Mary Ruth

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Query Match:
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SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 1152
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PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
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CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10
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TITLE OF INVENTION: OBG3 Globular Head and
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566 GCCGTTCTCTTCACCTACGACCAGTATCAGGAAAAGAATGTGGACCAGGCCTCTGGCTCT 625
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                                                                                                                                         TATGACAACAGCACTGGCAAGTTCTACTGCAACATTCCGGGGACTCTACTACTACTTCTCTTAC
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                                 ThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHis
                                                                                                                                                                                                              GAGCCTGGAGAAGCCGCTTATGTGTATCGCTCAGGCTTCAGTGTGGGGGCTGGAGACCCGC
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                                                                    CACATCACGGTGTAC----ATGAAAGATGTGAAGGTGAGCCTCTTCAAGAAGGACAAG
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SEQ ID NO 1
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CURRENT APPLICATION NUMBER: US/09/909,547
CURRENT FILING DATE: 2001-07-19
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PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
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TITLE OF INVENTION: OBG3 Globular Head and
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TYPE: DNA
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                                ---GlyGlnHisGlyProLysGlyGluLysGlyTyrProGlyIleProProGlu-----
                                                                      GGAGAGAAGGGAGAAAGGAGATTCAGGTCTTCTTGGTCCTAAGGGTGAGACAGGAGAT
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	686 CACAATGGACTCTATGCAGATAACGTCAACGACTCTACATTTACTGGCTTTCTCTTCTCTTC 745	AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPhe 243	626 GTGCTCCTCCATCTGGAGGTGGGAGCCAAGTCTGGCTCCAGGTGTATGGGGATGGGGAC 685	AlaValLeuLysLeuAlaLysGlyAspGluValTrpLeuArgMetGlyAsnGly 225	566 GCCGTTCTCCACCTACGACCAGTATCAGGAAAAGAATGTGGACCAGGCCTCTGGCTCT 625	188 ThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHis 207	512 CACATCACGGTGTACATGAAAGATGTGAAGGTGAGGCCTCTTCAAGAAGGACAAG 565	SerMetMetLysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187	TATGACAACAGCACTGGCAAGTTCTACTGCAACATTCCGGGACTCTACTACTTCTCTTAC 511	PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe 167	392 GTCACTGTTCCCAATGTACCCATTCGCTTTACTAAGATCTTCTACAACCAAC	PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 147	332 GAGCCTGGAGAAGCCGCTTATGTGTATCGCTCAGGCTTCAGTGTGGGGCTGGAGACCCGC 391	LeuGlnIleAlaPheMetAlaSerLeuAlaThrHis 127

Search completed: January 15, 2003, 21:23:46 Job time : 106 secs

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ALIGNMENTS

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RESULT 1
AAA96336
cDNA encoding a novel polypeptide designated PRO1484
                                                  08-FEB-2001 (first entry)
                                                                                                                                                   AAA96336 standard; cDNA; 1712 BP
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Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122; PRO1899; PRO1890; PRO1887; PRO4785; PRO4353; PRO44357; PRO4405; PRO4356; PRO4352; PRO4380; PRO4354; PRO40408; PRO5737; PRO4425; PRO5990; PRO6030; PRO4352; PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes; insulinemia; kidney disorder; Bergers disease; nephropathy; Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis; CDS sig_peptide Homo sapiens. Crohns WO200056889-A2 77. 817 /*tag= a 77..142 ocation/Qualifiers '*tag=

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The present sequence encodes a secreted or transmembrane polypeptide. CC The specification describes polypeptides designated PRO1484, PRO4334, CC PRO1122, PRO1889, PRO1899, PRO1887, PRO1785, PRO4333, PRO4357, PRO4405, CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4409, PRO5737, PRO4425, PRO5990, CC PRO6030, PRO4424, PRO4422, PRO4354, PRO4409, PRO1889 polypeptide is CC useful for diagnosing tumour in a mammal. The polypeptides, their CC expression or activity of the polypeptide. Condition associated with CC expression or activity of the polypeptide. Conditions treated include CC obssity, diabetes or hyper-or hypo-insulinemia. The polypeptides are CC capable of inducing proliferation of mammalian kidney mesangial cells CC decreased mesangial cell for treating kidney disorders associated with CC decreased mesangial cell function such as Bergers disease or other CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used to generate transgenic animals for use in development and screening of therapeutically useful reagents and also for chromosome identification covered by the condition of the condition 
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This sequence represents the cDNA for a human immune system molecule (IMOL) isolated as clone 1890540 from the Incyte BLADTUT07 library.

The human IMOLs (AAB15536-B15550) and their encoding polynucleotides (AAA95775-A95789), and compositions comprising them are useful for the
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                                                                                                New human immune system molecules 1-15 and polynucleotides encoding them useful for diagnosing, treating or preventing e.g. immunological disorders, infections, cell proliferative disorders, microbial
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                             TGAGGAAGTGTATGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA
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Query Match Best Local | Matches 169

Similarity

99.1%;

Score 1696; Pred. No. (

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Conservative

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Mismatches

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CC The invention relates to the human zacrp3 protein (AAB29580) and to CC nucleic acids which encode it (AAC64058), AAC64063). Zacrp3 is a homogue CC of adipocyte complement related protein (ACRP30) and contains a CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a CC terminal Clq domain comprising 10 beta-strands. The zacrp3 gene is CC located on chromosome 5p12. The invention also relates to zacrp3 gene is CC ragments, fusion proteins containing zacrp3 polypeptides, CC zacrp3-specific antibodies, expression constructs and host cells CC comprising zacrp3 nucleic acids, and methods of recombinant production of CC cacrp3. Human zacrp3, and its agonists and atagonists may be used in the CC study and modulation of cellular metabolism and energy balance in CC mammals, and may therefore be used to treat disorders such as obesity and CC carpains, and conditions associated with these disorders. Due to its Clq Clike domain, zacrp3 and zacrp3-containing fusion proteins may be useful CC as antimicrobial agents, promoting lysis or phagocytosis of infectious cryanisms such as bacteria or viruses. Zacrp3, its fragments, fusion proteins, antibodies and activity modulators may also be used to inhibit CC collagen-induced platelet aggregation, adhesion, or activation, and may therefore have potential for promoting blood flow within the vasculature CC dimerisation and oligomerisation. The present sequence represents cDNA cc encoding human zacrp3 and its antibodies may additionally be used to study constanting human zacrp3 and present sequence represents cDNA constanting human zacrp3.
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11-JAN-2000;
02-MAY-2000;
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Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development -
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                                                                                                                                                                                                                                                                                    07-JUL-2000;
                                                                                                                                                                                                                                                                                                                            10-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secretory protein; membrane rheumatoid arthritis; diabetes; ss.
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                                                                                                                                                               (HELI-)
                                                            2001-093989/11.
DB; AAB88447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCACTTTTGATCACATACAATACATTAAAAGTCACTTTTGATCACATACAATACATTAAAAGTCACATACAATACAATACAATACATTAAAAGTCACATACAATACAATGCTATTTTAAAGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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; 2000JP-0118775.
; 2000JP-0183766.
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Best Local Similarity 99.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid artivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate to cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1709 BP; 480 A; 363 C; 390 G; 476 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis and
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                                                                                                                                                                                                                                                                                                                     AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT 600
                                                                      AGGGGAGCGGGGCAGCATGGCCCCAAAGGAGAAGGGCTACCCGGGGATTCCACCAGA 420
                                                                                                                                                                                                                                                                                                                                                                            CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 312
                                                                                                                                                                                                                                                                                                                                                                                                               CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCCTACCAAGGCCC
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                                                                                                                                                ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT 480
                                                                                                                                                                                                                                                                                                    AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCATCTGCCCGAGGAGACCACGCTCCCGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 72
                                                                                                                                                                                                                          AGGGGAGCGGGGCAGCATGGCCCCAAAGGAGAGAGGGCTACCCGGGGATTCCACCAGA 432
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Pred. No. 0;
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                   ATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA 1692
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γQ	601	GAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACACTCTTCAGCATGTACAGCTA 66	0
뮹	613	AGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA 67	2
Qy		TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 72	0
Ф	673	GAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 73	2
Qy		TGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCT TCTC 78	0
В	733	GATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTC 79	Ñ
Qγ	781	ACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC 84	0
DЪ	793	TGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC 85	ν
Qγ	841	TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 90	ō
ф	853	TTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 91	2
 Οу	901	GTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACA 96	0
DЪ	913	TTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACA 97	Ν
Ωу	961	CCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA 10	20
DЪ	973	CANTAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA 10	32
Qy	1021	TGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAAT 10	80
DЪ	1033	GACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAAT 10	92
Qy		TCTCCTCTGACGCAGGTTGGAAATATTTTTTTTCTATCACAGAAGTCATTTGCAAAGAATT 1	40
Db	1093	CTCCTCTGACGCAGGTTGGAAATATTTTTTTTCTATCACAGAAGTCATTTGCAAAGAATT 11	52
Qy	1141		00
Db	1153	TGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA 12	12
Qy	1201	GTGATATGACAGGGCTGGGGCAAGAA 12	60
Db .	N	TATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAA 12	72
ОУ	N	CTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTG 13	20
ДD	1273	AGGGGCACTAGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCCTTAGCCTTTG 13	32
Qy	1321	ACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTT 13	80
Db	1333	CCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTT 13	92
Qy	1381	TAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTTGTGT 14	40
Db	(.)	AAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGT 14	52
Qy	1441	Ġ	00
Db	-	TGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATT 15	12
Qy	1501		60
Db	Ċ	ACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATG 15	72
Qy	1561	TTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATA	20
Db		TGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATA	32
Qy		ATTTTGACCTGCCTTTAGATAAAACTGTGGCAAGAAAATGTAATGAGCAATATATGGAA 16	80
7	1622	TTTTTCACCTTTTACATAAAACTCTTCCCAACAAAATCTAATCACCAATATATCCAA 16	S

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04-FEB-2000;
24-FEB-2000;
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14 - AUG -
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14-AUG-2000;
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17-MAR-
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30-JUN-2000;
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2000US-0179065
2000US-0188628
2000US-01886350
2000US-0188874
2000US-0198123
2000US-0198123
2000US-029467
2000US-0216886
2000US-0216886
2000US-0217496
2000US-0217496
2000US-0217496
2000US-0217496
2000US-0217496
2000US-0217496
2000US-02252963
2000US-0225214
2000US-0225214
2000US-0225214
2000US-0225266
2000US-0225344
2000US-0225759
2000US-0225759
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2000US-02259343
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2000US-0232081.
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2000US-0232081.
2000US-0232981.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained no electronic format directly or the sequence in the printed parasitic infections.
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Best Local Similarity

Matches 1549; Conserv
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17-NOV-2000
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06-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids and polypeptides, useful for treating, preventing ameliorating human disorders and diseases \cdot
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P-PSDB; AAM99925.
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                ACAAAGGTGACCTGGGGCCTCGAGGGGGAGCGGGGCAGCATGGCCCCAAAGGAGAGAAAGG
                                                ACAAAGGTGACCTGGGGGCCTCGAGGGGGAGCAGCATGGCCCCAAAAGGAGAAAGG
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Pred. No. 0;
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1479 CAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCA 1538
                               1282 TAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGCGGT
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1478	TAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGT		Qy
1281	ATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACC	2	Дb
1418	AATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAA	S	Оу
1221	TCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATKCATTAAAACTCTTCCGTGTTCAGCACATAACACTCTTCCCTTTTGATCCACAAAATACATTAAAACTCTTCCGTGTTCAGCACAAAATACATTAAAAACTCT	1162	Дb
o i⊢	ATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCC	10) Db
	TATGACAGGGCTGGGGCAAGAACAGGGGGCACTAGCTGCCTTATTAGTAGCTAATTTAGTGCCC	1239	. Oy
1101	TTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCAGATGTAGTG		Db
	ACCCCTGAAGTTTTAAGTTCATTATTCTTTATAAC	17	Qy
1041	CAGAAGTCATTTGCAAAGAATTTTGACTRCTCTGCTTTTAATTTTAATACCAGTTTTTCAGG	982	Db
1178	AGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAG	1119	Оу
981	TCTATCA	922	Db
1118	CCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCA	1059	Qy
921	AATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCACTC	862	Db
1058	CCACAAAATAGTCTTCTCAGATGACCTTGACTAATATAC	999	Qy
861	GTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATC		Дb
	TGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCA	939	Qy
	GGTTGCA	742	Db
938	AGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAAATTATTGGTTGC	879	Qy
741	_	682	DЬ
7	ATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGAT	819	Qy
681	ATGGGGACCACCACCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAA	622	Db
818	TGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAA	759	Qy
621	CTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCC	562	Db .
758	GTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTC	699	Qy
561	CTATGAAATGAAGGGCAAATCA	502	DЬ
869	AGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCAT	639	Оy
501	GCAACA	442	Db
638	ATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTATCCATATGCACAATGGCAACA	579	Qy
441	TGTGTATTTCTTCACCTTCA	382	Db
578	GATGTCATGACTGGTAGATTTGGGGCCCCCAGTATCAGGTGTGTATTTCTTCACCTTC	519	Qy
381	TCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCT	322	Db
518	CAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCT		Оу
321	GCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACT	262	Db
458	CTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACT	399	Qy

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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Wang
Zhao
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leukaemia; ss.
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                                                                                                          Claim
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                                                                                                                                          Novel
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DB; AAM40074.
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                                                                                                                                        nucleic acids and
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Wang 2
Zhou
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2000US-0553317.
2000US-0598042.
2000US-0620312.
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system injuries -
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Yang Y,
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Zhang v
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Note: The sequence data for this patent did not form part of the specification.
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ATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCAC 1054
                                        GCAATGTTGTTCACGCTACAGGTACACACAATAATGTTGGACAATTCAGGGGCTCAGAAGA
                                                                             CGATCTGAGGAACATTAAAGTTGAGGGTTTTTACATTGCTGTATTCAAAAAATTATTGGTT
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                                                                     CGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTT
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                              GCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCCTCAGAAGA
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                                                                                                     haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; Chemotactic; Chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic; contraceptive; antiinfertility; antiinflammatory; ss.
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               sig_peptide
                                                                                                                                             cell proliferation; immunomodulatory; autoimmune disorder; antimicrob multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
                                                                                                                                                              Human; hydrophobic domain; gene therapy; nutritional supplement;
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/product= "Human p
/note= "CDS is specared by...157
/*tag= b
                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                  having hydrophobic domain encoding cDNA clone
                                                       Location/Qualifiers 89..760
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                          specifically is
                           y hydrophobic domain"
claimed in claim 3"
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ACAAAGGTGACCTGGGGGCCTCGAGGGGGAGCGGGGGGCAGCATGGCCCCCAAAGGAGAGAAGG

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ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGCCG

ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG

AGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACA 218

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                                                                                                                                                               The present sequence is human protein with hydrophobic domain encoding CC cDNA clone Hp10781. The polynucleotide and polypeptide of the invention CC may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate polypeptide expression. The polynucleotides CC into a host cell and culturing the cell to express the protein. The cC into a host cell and culturing the cell to express the protein. The CC polypucleotides and its complementary sequences may also be used as DNA CC probes in diagnostic assays and also used in gene therapy. The CC and in assays to identify modulators of polypeptide expression and CC supplements, to modulate cytokine and cell proliferation activity, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of CC microbial infections and autoimmune disorders such as multiple sclerosis, temmatoje arthritis and insulin-dependent diabetes), to modulate condulate tissue growth activity (e.g. for the treatment of CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's CC disease), to modulate activin and inhibin activity, to modulate creciptor CC modulate haemostatic and thrombolytic activity, to modulate receptor CC ligand activity, to modulate inflammation and to inhibit tumour growth.
   Best Loc
Matches
                                                        Query Match
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06-JAN-2000;
11-JAN-2000;
03-FEB-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, \, Alzheimer's and inflammation -
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(SAGA)
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                                                                                                                    TCCGTGTTCAGCTTAGCCTTTGACCCTTTTCATCCACAAAATACATTAAAACTCT
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TAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGT
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                                                     GAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAG
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                                                                                                                                                                                                                                                                         Human; secreted protein; gene; ss; nutritional supplement; haemophilia; viral infection; bacterial infection; fungal infection; diabetes; asthm: autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour; autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer coagulation disorder; inflammatory disorder; Crohn's disease; incision; tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency.
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Homo

18-OCT-2001

29-MAR-2001; 2001WO-US10224

06-APR-2000; 2000US-195582P

(GEMY) GENETICS INST

Gulukota K, Wong GG, Clark HF, Graham Fechtel JR; ζ, Agostino 3 Howes SH, Resnick ŖJ;

WPI; 2002-179321/23

Five hundred and ninety two polynucleotides human tissue sources which encode secreted preacting immune deficiencies and disorders: s derived from a var proteins, useful fo such as autoimmune variety for disorders of.

Claim 1; Page 261-262; 372pp; English

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The invention relates to 592 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins. The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and tumours. They are also

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1365; Conserv
                                                           TTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT
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                          GGAACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGT
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KW Ieukaemia
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PN W02001533
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PD 26-JUL-20
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PR 25-APR-20
PR 25-APR-20
PR 19-JUL-20
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukacentia.
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DB; AAM41860.
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                                                                Liu C
Wang Z
Zhou
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0639036.
2000US-0727344.
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Wehrman T, X
Goodrich R,
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                                                                                                                                                                                                                                                                                                                             GGCAACCCACTTCAGCAATCAGAACAGTGGGGATTATCTTCAGCAGTGTTGAGACCAACAT
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                                                               TGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGA
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The sequence data for this patent did not form part of the printed
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93.6%;
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Human; secretory protein; rheumatoid arthritis; dial

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CC AAB8317 - AAB8419. Included in the invention are primers
CC AAF93917 - AAF64295 and AAF62232 - AAF62235 which are used to isolate the
CC CDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC used to study the expression and function of secretory proteins/membrane
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies and antagonists may also be used as diagnostic agents for detecting the presence of the
CC used to study the expression and activity. The antibodies may also
De used as diagnostic agents for detecting the presence of the
CC agents to down regulate expression and activity. The antibodies may also
De used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC arthritis and diabetes.
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Best Local :
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02-MAY-2000;
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or as candidate target molecules in drug development
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                                      Agarwal P, Smith RF,
                                                                                                                                                                                                                        Human; secreted protein; membrane-associated protein; hypertension; inflammatory disorder; neurological disorder; haematopoietic disord skeletal developmental disorder; growth abnormality; autoimmune dis neurodegenerative disorder; nervous system disorder; bacterial infeperipheral myelinopathy; viral infection; cancer; obesity; diabetes hypotension; sexual development disorder; blood disorder; gene; ds.
          WPI; 2002-188468/24.
P-PSDB; AAU84371.
                                                                    (SMIK )
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21-AUG-2000;
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2000US-226517P
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                                                                                                                                                                                                                                                                                                protein #10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypotension, obesity, bulimia, anorexia, manic depression, delirium, mental retardation, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade system including those leading to stroke. ABK35587-ABK35609 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or membrane-associated proteins and
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                                                                                                                                                    GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTTGGGGCCCCAGTATCA
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                                                                                                                                                                                                                                                                                                    mammalian skin cells. The polypeptide is useful for stimulating mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide used in the identification disorders and encoding polypeptides used for treating disease, cancer and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         keratinocyte growth stimulation; cancer; amunomodulatory; inflammation; neurological disease. es
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    neuroprotective: vulnerary: immunomodulatory
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                                                                                                                                  AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG
                                                                                                                                                                                                                                  CTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTA
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                                                                                                               AGAATCAACCACAAAATAGTCTTCTCAGA 1020
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                                                                                                       AGAATAGACCACAAGGTAATATTCCCAGA 1035
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                                                                   standard;
 defect; inflammatory disease;
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                       SEQ
                       ID NO:
       cancer;
ancer; growth defect;
dermatological; vulnerary;
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immunomodulator;
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               anti-inflammatory; cytostatic;
               neuroprotective;
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WO200190357-A1 29-NOV-2001

24-MAY-2000; 25-JUL-2000; 24-MAY-2001; 2000US-206650P. 2000US-221232P. 2001WO-NZ00099

(GENE-) GENESIS RES & DEV CORP LTD

Watson 2002-122020/16 a Ļ Sleeman ž Onrust R, Murison JG, Kumble

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New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for modulating immune responses

Claim 1; Page 262; 466pp; English.

The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound have important modulating immune responses. The present sequence is a new large that in modulating immune responses. The present sequence is a invention.

Sequence 1035 BP; 255 Α; 242 C; 298 G; 240 T; 0 other;

Query Match Best Local Sin Matches 819; Similarity 82.8 19; Conservative 40.7%; 82.8%; 0; Score 696.2; Pred. No. 5.1 Mismatches .1e-192; DB 24; Indels Length 1035 2; Gaps ?

48 ယ္ 93 CTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGCAGC 107

228 ATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGTCCTCCTGGCATTCCAG ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 287

288 273 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA

393 348 407

453 CCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 467

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                                                                                                                                        04-NOV-1999
                                                                                                                                                                                                                                              Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying c secreted; transmembrane; inflammation; cancer; neurological disea
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         WPI; 2000-072177/06
                                                                                29-APR-1998;
09-NOV-1998;
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                                                                                                                                                                                                             anti-inflammatory;
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                                 Sleeman
                                                                                                                                                                                                                                                                                             rat skin cell secreted protein,
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98US-0188930.
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                                                        RES & DEV CORP LTD.
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Novel polynucleotides useful for including wounds and cancer -Claim 1; Page invention relates English. the treatment of various conditions

dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, cc and mouse embryonic skin, keratinocytes tem cells and transit amplifying cc cells. Polypeptides of the invention may be used to treat inflammation, cc cancer and neurological diseases. The proteins may be used to stimulate cc the growth and motility of keratinocytes, to inhibit the growth of cc cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to cc inhibit binding of HIV-1 to leukocytes. The invention may also be used cc inhibit binding of HIV-1 to leukocytes. The invention may also be used cc disorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived cc from several mouse, rat or human skin cell types. Sequences aZ61606-Z61606-Z61602-Z61811 and AAZ61826 encode cc proteins with an N-terminal signal sequence, indicating that the proteins can daZ61827-Z61819 encode proteins with a N-terminal signal sequence, indicating that the proteins and AAZ61827-Z61819 encode proteins with one or more putative transmembrane domains. to novel nucleic acid sequences derived from rat keratinocytes and neonatal foreskin fibroblasts, kin, keratinocyte stem cells and transit amplifying

Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Query Match Best Local S

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Length

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GTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAATCAGATACATCCAGCA

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RESULT 15
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and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to
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anti-inflammatory;
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                                                                               The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
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                                                                                                                                                                                                                                                                                                                          29-APR-1999;
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                                                                                                                                                 Novel polynucleotides including wounds and
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DB; AAY76025.
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logical disease;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1123 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibit binding of HIV-1 to leukocytes. The invention may also be to treat growth and developmental defects, skin wounds and hair
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                                    AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG
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                                                                                                                                         ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGCCAATGGCC
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10 US-09-878-1716

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10 US-09-738-973-151

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10 US-09-776-976-5
                             US-09-758-055-5

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Sequence 12152, A
Sequence 28732, A
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Sequence 1716, Ap
Sequence 151, App
Sequence 151, App
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US-09-800-729-44	US-09-800-729-48	US-09-789-561-82	US-09-800-729-45	US-09-880-107-2094	US-09-954-456-786	US-10-098-841-182	US-09-925-302-152	US-09-800-729-46	US-09-925-299-44	US-09-800-729-47	US-09-800-729-14	US-09-925-302-247	US-09-909-547-1	US-09-758-055-1	US-09-776-976-1	US-09-964-824A-255	US-09-954-531-961	US-10-052-586-331	US-10-176-758-331	US-10-174-590-331	US-09-978-189-613	US-09-999-832A-613	US-09-978-192A-613	US-09-978-697-613	US-09-978-295A-613	
Sequence 44, Appl	Sequence 48, Appl	Sequence 82, Appl	Sequence 45, Appl	Sequence 2094, Ap	Sequence 786, App	Sequence 182, App	Sequence 152, App	Sequence 46, Appl	Sequence 44, Appl	Sequence 47, Appl	Sequence 14, Appl	Sequence 247, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 255, App		Sequence 331, App	•	Sequence 331, App	•	Sequence 613, App	•	Sequence 613, App	Sequence 613, App	

ALIGNMENTS

RESULT 1 US-10-036-041-1

Sequence 1, App Publication No.

Application US/10036041 No. US20020192751A1

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PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3030R1C8
CURRENT FILING NUMBER: US/10/036,041
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
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                                                                            PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
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                       APPLICATION NUMBER: 60/125774 FILING DATE: 1999-03-23
APPLICATION NUMBER: 60/125778
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OR FILING DATE: 2001-02-28
OR APPLICATION NUMBER: PCT/US01/17800
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OR APPLICATION NUMBER: PCT/US01/19692
OR FILING DATE: 2001-06-20
OR APPLICATION NUMBER: PCT/US01/21066
OR APPLICATION NUMBER: PCT/US01/21735
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DR FILING DATE: 1999-05-14

DR APPLICATION NUMBER: PCT/US99/28551

DR FILING DATE: 1999-12-02

DR APPLICATION NUMBER: PCT/US99/30720

DR FILING DATE: 1999-12-22

DR APPLICATION NUMBER: PCT/US90/05601

DR FILING DATE: 2000-03-01

OR FILING DATE: 2000-03-01
OR APPLICATION NUMBER: PCT/US00/05841
OR FILING DATE: 2000-03-02
OR APPLICATION NUMBER: PCT/US00/14042
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OR APPLICATION NUMBER: PCT/US00/23522
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OR APPLICATION NUMBER: PCT/US00/2328
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OR FILING DATE: 2000-12-01
OR APPLICATION NUMBER: PCT/US00/32678
OR FILING DATE: 2000-12-01

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OR FILING DATE: 2001-03-22
OR APPLICATION NUMBER: 09/854208
OR FILING DATE: 2001-05-10
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OR FILING DATE: 2001-06-05
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OR APPLICATION NUMBER: 09/96959
OR FILING DATE: 2001-06-29
OR FILING DATE: 2001-06-29
OR APPLICATION NUMBER: 09/908,827
OR APPLICATION NUMBER: 09/908,70733
OR APPLICATION NUMBER: 07/US99/10733

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OR APPLICATION NUMBER: 60/13279
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OR APPLICATION NUMBER: 60/13233
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OR FILING DATE: 1999-05-25
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OR FILING DATE: 1999-06-08
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OR APPLICATION NUMBER: 09/3144484
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RESULT 2
US-10-035-855-1
; Sequence 1, Application US/10035855
; Publication No. US20030008348A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

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APPLICANI: Goddard, Nudrey

APPLICANI: Gurney, Austin L.

APPLICANI: Godowski, Paul J.

APPLICANI: Stewart, Timothy A.

APPLICANION NUMBER: 60/08579

PRIOR ELILAN DATE: 1999-05-15

PRIOR PILLA DATE: 1999-12-23

PRIOR PILLA TIMO STEE: 1999-13-24

PRIOR PILLA TIMO STEE: 1999-13-24

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PRIOR PILLA DATE: 1999-13-24

PRIOR PILLA DATE: 1999-13-25

PRIOR PILLA DATE: 1999-13-26

PRIOR PILLA
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; NUMBER OF SEQ ID N

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; LENGTH: 1712

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ICR FILING DATE: 2000-03-01
ICR APPLICATION NUMBER: PCT/USO0/05841
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ICR FILING DATE: 2000-05-02
ICR FILING DATE: 2000-06-02
ICR FILING DATE: 2000-06-02
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ICR FILING DATE: 2000-08-24
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FILING DATE: 1999-05-14
APPLICATION NUMBER: PCT/US99/28551
FILING DATE: 1999-12-02
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FILING DATE: 2000-12-20
APPLICATION NUMBER: 09/816744
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32 32	TATTCTTTAIPACATTTGAGAGATCGGAIGTAGIGATATGACAGGGCIGGGGCAAG AGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCTCCGTGTTCAGCTTAGCCTI 	WNNN	oy og
1260	TATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAA	1201	Dy Oy
1200 1200	TIGACTACTCTECTTITAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA	1141 1141	Оy
1140 1140	TCTCCTCTGACGCAGGTTGGAAATATTTTTTTTTATCACAGAAGTCATTTGCAAAGAATT	1081	Оу
1080 1080	TGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAAT	1021	Qу Db
1020 1020	CCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA	961 961	Фр
960	GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACAGITACA	901 901	Qу Db
900	TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 	841 841	Qу Db
840 840	CACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC	781 781	Фр
780 780	GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTC	721 721	Qy Db
720 720	TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 	661 661	Qy Db
660	TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA	601	Qy
600	TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT	541 541	Qy Db
540 540	TATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGCTAGATT		Qy Db
480 480	ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT		Qу
420 420	AGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAGAGGCTACCCGGGGATTCCACCAGA	. 361 361	Оу
360 360	AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCCACAAAGGTGACCTGGGGGCCTCG	301 301	Db .
300	CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG	241 241	D Qy

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GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Pan, James
APPLICANT: Stewart, Timoth
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PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR APPLICATION NUMBER: 60/113300
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CURRENT FILING DATE: 2001-12-26
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OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/113605
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/113621
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/114140
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FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/116843
FILING DATE: 1999-01-22
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FILING DATE: 2000-12-20
APPLICATION NUMBER: 09/816744
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FILING DATE: 1999-05-14
APPLICATION NUMBER: 09/380142
FILING DATE: 1999-08-25
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APPLICATION NUMBER: PCT/US00/34956
FILING DATE: 2000-12-20
APPLICATION NUMBER: PCT/US01/06520
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OR APPLICATION NUMBER: PCT/US01/21066
OR FILING DATE: 2001-06-29
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US-09-822-849A-359
; Sequence 359, Application |
; Patent No. US20020045170A1
; GENERAL INFORMATION:

US/09822849F

APPLICANT: Wong, Gordon G APPLICANT: Clark, Hilary APPLICANT: Fechtel, Kim APPLICANT: Agostino, Micl APPLICANT: Howes, Steven

Fechtel, Kim Agostino, Michael Howes, Steven H.

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; LENGTH: 1608
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LENGTH: 1608
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APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
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PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
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Gulukota, Kamalakar
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: PCT/US01/00666
PRIOR PPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30 Sequence 12152, Application Patent No. US20020048763A1 GENERAL INFORMATION: PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23 APPLICANT: APPLICANT: Penn, Sharron FILE REFERENCE: Aeomica-X-1 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGITIELE OF INVENTION: GENE EXPRESSION ANALYSIS APPLICANT: Rank, David R. Hanzel, David K Chen, Wensheng <u>.</u>~ US/09864761 SINGLE EXON NUCLEIC LYSIS BY MICROARRAY ACID PROBES USEFUL

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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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SOFTWARE: Au..
TO ID NO 12152
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Best Local Similarity
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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ORGANISM: Homo sapiens
FEATURE:
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5. US20020048763A1
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EXPRESSED IN BONE MARROW, SIGNAL = 0.83

EXPRESSED IN LUNG, SIGNAL = 1.1

EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

EXPRESSED IN BRAIN, SIGNAL = 0.82

EXPRESSED IN PLACENTA, SIGNAL = 1.1

EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
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Pred. No. 4.4e-28;
0; Mismatches 3
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                                                        GENERAL INFORMATION:
                                                                            Sequence 1716, Application Patent No. US20020156011A1
  APPLICANT: Jiang, Yugiu
APPLICANT: Harlocker, APPLICANT: Secrist, He
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-864-761-28732
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 49117
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TYPE: DNA
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-29
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                                                                                          AGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCC 547
CCAGTATCAG 130
                                                                        AGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGGCC
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NN: EXPRESSED IN BONE MARROW, SIGNAL = 0.83

NN: EXPRESSED IN LUNG, SIGNAL = 1.1

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

NN: EXPRESSED IN BRAIN, SIGNAL = 0.82

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.1

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96

NN: NT HIT: U29581.1, EVALUE 2.90e-01

NN: SWISSPROT HIT: P98087, EVALUE 2.70e-01

NN: EST_HUMAN HIT: AA334609.1, EVALUE 2.00e-67
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Secrist, Heather

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APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
IITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FAStSEQ for Windows Version 4.0
SEQ ID NO 1716
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TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1716
SEQ ID NO 1716
LENGTH: 432
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Best Local Similarity 52.4%;
Matches 173; Conservative
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                                                                                            Query Match
Best Local :
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APPLICANT:
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                                                                                                                                                                                           LENGTH: 432
TYPE: DNA
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Local Similarity 52.4%;
hes 173; Conservative
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  ATTGTGTTTGATCTTCTGGAACAACTTAGGAGAAACTTTTGATCTTCAGCTTGGTAGA 148
                    ATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGA 538
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Stolk, John A.
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                                                                        Score 78.8; DB 9;
Pred. No. 3.8e-12;
0; Mismatches 157;
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Pred. No. 3.8e-12;
0; Mismatches 157;
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-151
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LENGTH: 3275
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Best Local Similarity
Matches 173; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
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  2745
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                                        TCCACCTTTGCAGGATTCCTGCTCTTTGAA 808
                                                                                  GGAGACCAGATATGGTTACGTCTGCACAGGGGAGCAATTTATGGAAGTAGCTGGAAATAT 2744
                                                                                                                          GGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCCAACGCTTC 778
  TCTACGTTTTCAGGCTATCTTTTATCAA 2774
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Pred. No. 1.4e-11;
0; Mismatches 157;
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TYPE: DNA
ORGANISM: Homo sapien
US-09-738-973-151
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US-09-738-973-151
                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                  Sequence 5, Application US/09776976 Patent No. US20020037849A1
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Best Local Similarity
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                                                      APPLICANT: Fruebis, Joachim
APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. US20020110563A1
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CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
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CURRENT FILING DATE: 2000-12-14
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Kalos, Michael D.
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Indirias, Carol Yoseph
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Pred. No. 1.4e-11;
0; Mismatches 157;
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                                          US-09-758-055-5
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PRIOR APPLICATION NUMBER: US-60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US-60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
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Matches
Sequence 5, Application US/09758055 Patent No. US20020058617A1
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SEQ ID NO 5
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Pred. No. 2.5e-10;
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SEQ ID NO 5 PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13 CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10 APPLICANT: Bihain, Bernard TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass FILE REFERENCE: 76.US4.REG NUMBER OF SEQ ID NOS: SOFTWARE: Patent.pm PRIOR APPLICATION NUMBER: US 60/299,881 PRIOR FILING DATE: 2000-09-01 APPLICANT: ORGANISM: Homo sapiens TYPE: DNA ENGTH: 4517 Yen, Frances GENERAL INFORMATION:

APPLICANT: Fruebis, Joachim

APPLICANT:

US-09-758-055-5

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US-09-909-547-5
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US-09-909-547-5
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Matches 210; Conserval
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                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                              SEQ ID NO 5
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR APPLICATION NUMBER: US 60/176,228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and
FILE REFERENCE: 76.US6.CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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PRIOR FILING DATE: 2001-02-05
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                                                                  Score 74.6; DB 10;
Pred. No. 2.5e-10;
0; Mismatches 204;
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US-09-964-824A-235
; Sequence 235, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
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; ORGANISM: HOMO
US-09-964-824A-235
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CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
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LENGTH: 4517
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Best Local Similarity 50.48;
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                    456
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; LENGTH: 1276
; TYPE: DNA
; ORGANISM: mus musculus
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PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
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CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
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TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
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	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF326976	RESULT 1
of the human CORS26 gene	Molecular cloning, chromosomal localization, and genomic structure	Maeda, T., Hayashi, A. and Saito, T.	1 (bases 1 to 1730)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens.		AF326976.1 GI:14586742	AF326976	Homo sapiens putative secretory protein CORS26 mRNA, complete cds.	AF326976 1730 bp mRNA linear PRI 03-JUL-2001		

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/protein_id="AAK70344 1"
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PKCEKGYPGIPPELQIARMASLATHFSKNONSGIIFSSVETNICNFFDVMTGREGAPVS
GVYFFTESMMKHEDVEEVYVYLMHONTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEV
WLKHGNGALHGDHQRFSYFAGFILLFETK"

### MLMROLITER ### MLM
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GCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTTGGTAGATTTGGGGCCC
                                      TTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCA 488
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AX039945 GI:11229969
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Piddington,C.S. and Bishop,P.D.
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GDYSFRGYQGPDEPGDPGIPGHKGNNUNNGATGHEGAKGEKGDKGDLGFGERGQHG
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GVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEV
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DЬ	481 GCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCC 540	J
Qy	CAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGAAGCATGAGGATGTGAGGAAG 60	æ
DЬ	CAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAG 60	Ō
Qy	TGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGA 66	8
ф	TGTATGTGTACCTTATGCACACATGGCAACACACTCTTCAGCATGTACAGCTATGAAATGA 66	0
Qy	AGGGCAAATCAGATACATCCAGCÁATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGG 72	8
рь	AGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGG 72	0
Qy	TTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCCACCTTTG 78	80
DЬ	TTTGGCTGCGAATGGCGATGGCGCTCTCCATGGGGACCAACGCTTCTCCACCTTTG 78	0
Qy	CAGGATTCCTGCTCTTTGAAACTAAGTAAATATGACTAGAATAGCTCCACTTTGGGGA 84	8
DЬ	CAGGATTCCTGCTCTTTGAAACTAAAGTAAATATGACTAGAATAGCTCCACTTTGGGGA 84	0
Qy	AGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACA 90	8
дb	AGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGGAACATTAAAGTTGAGGGTTTTACA 90	0
Qy	TTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAAT 96	00
, Dp	TTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAAT 96	0
Qy	GTTGGACAATTCAGGGGCTCAGAAGAATCAACCAAAATAGTCTTCTCAGATGACCTTG 10	28
ф	GTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGATGACCTTG 10	20
Qy	ACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAATTCTCCCTCT 10	88
Db	021 ACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAATTCTCCTCT 10	80
Qy	9 GACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATTTTGACTAC 11	48
Db	081 GACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATTTTGACTAC 11	40
Qy	149 TCTGCTTTTAATTTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCATTATTCTT 12	80
Db	141 TCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTAAGTTCATTATTCTT 12	00
Qy	209 TATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAACAGGGGCA 12	89
Db	201 TATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAACAGGGGCA 12	60
Qy	269 CTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCCTTAGCCCTTTGACCCTTTC 13	28
Db	261 CTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTGACCCTTTC 13	20
Qy	329 CTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCA 13	88
Db	321 CTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCA 13	08
Qy	ATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGTATGTTCCC 14	48
ф	381 ATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGTATGTTCCC 14	40
Qy	449 CCACATCGCCCCCAACTTCGGATGTGGGGGTCAGGAGGTTGAGGTTCACTATTAACAAATG 15	80
Db	441 CCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATTAACAAATG 15	00
Qy	509 TCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAG 15	8
Db	501 TCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAG 15	60
Qy	69 AGGGATTTTATATCTGAAGAACATACACTATTAATAAATA	28
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Oy 8 GCCCGAGGACCACGCTCCTGGACCTCTCTCTCAGGGACACTCTCAGGCTCTG 1111111111111111111111111111111	Query Match 99.1%; Score 1696; DB 9; Length 1710; Best Local Similarity 100.0%; Pred. No. 0; Matches 1696; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	GDYSEKGYQGPPGPPGJPPGLIOINHONNGATGHGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	/codon_start=1 /product="complement-c1q tumor necrosis factor-related protein" /protein id="AAK17961.1" /protein_id="AAK17961.1" /db_xref="GI:13274520" /translation="MLWRQLIXWQLIALFFLPFCLCQDEYMESPOTGGLPPDCSKCCH	/gene="CTRP3" /note="ZACRP3" CDS 84. 824 /gene="CTRP3"	/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="3" /map="5p13-p12"	tle, WA	Unpublished 2 (bases 1 to 1710) Piddington, C.S. and Bishop, P. Direct Submission	Mammalla; EUCHETIA; FILMACES; 1 (bases 1 to 1710) Piddington,C.S. and Bishop,P. Homo sapiens complement-clq tu	txt	ON Homo sapiens complement-ciq cumor necrosis (CTRP3) mRNA, complete cds. N AF329837 AF329837.1 GI:13274519	AF329837 . 1710 bp mRNA linear PRI 12	Qy 1689 ACCTTTGTTAAAGATA 1704	Qy 1629 CTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAAATAAACAC 1688
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61 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 120
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                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1709)
Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
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Sequence 261 from Patent EP1067182.
AX136339
AX136339.1 GI:14272745
                                                                                                                                                                                                                                                                                                                                                                Secretory protein or membrane protein
Patent: EP 1067182-A 261 10-JAN-2001;
Helix Research Institute (JP)
Location/Qualifiers
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GVYFFTFSMMKHEDVEBVYVYLMHNGRTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEV
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89. .829
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1200	TTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA	1141	Qy
1140 1152	TCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATT	1081	Оу
1080 1092	TGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAAT	1021 1033	Оу
1020	CCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA	961	Qу
1032		973	рь
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972		913	ДЬ
900	TTTGGGGAAGACTTGTAGCTGAGCTGAGTTTGTTACGATCTGAGGAACATTAAAGTTGAGG	841	Оy
912		853	
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792		733	Db
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612		553	Db
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552		493	Db
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432		373	Db
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372		313	Db
300	CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG	241	Qy
312		253	.Db
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252		193	Db
180	TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT	121	Qy
192		133	Db
132		73	Db

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REFERENCE
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1 (bases 1 to 1927)

- s and Kimura, T.
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|ATAAACACACCTTTGTT 1709
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Sequence 59
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Patent: V
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DKGDLGPRGERGQHGPKGEKGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIG
NFLMS*
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Primates;
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WO0149728.
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                                                                                                                                                                                                                                                                                                                                                                                              BC016021 1426 bp mRNA linear PRI Homo sapiens, Similar to complement-clq tumor necrosis factor-related protein; likely ortholog of mouse CORS26 (collagenous repeat-containing sequence of 26 kDa proteingC:77511 IMAGE:4720611, mRNA, complete cds.
                                                               CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadanésystemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Forgreene, Mark Ketteman and Anuradha Madan
                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/bb_xref="GI:16359109"

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FTFSMMKHEDDVEDVYVYLMHRONTVFSNYSYEMKGKSDTSSNHAVLKLAEGDEVWLRM

GNGALHGDHQRFSTFAGFFLLFETK"
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/tissue_type="Placenta"
/clone_lib="NIH_MGC_79"
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Submitted (23 MAR-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
3 (bases 1 to 155013)
DOE Joint Genome Institute.
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gu
                                Direct Submission
Submitted (07-MAR-2002) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
On Mar 7, 2002 this sequence version replaced
------Genome Center
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Consensus quality: 154674 bases at least Q30
Consensus quality: 154674 bases at least Q30
Consensus quality: 154871 bases at least Q30
Estimated insert size: 171000; pulse field gel estimation
Estimated insert size: 154913; sum-of-contigs estimation
Quality coverage: 9.64 in Q20 bases; pulse field gel estimation
Quality coverage: 10.64 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs-of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 678 15013: contig of 6677 bp in length
* 678 15013: contig of 6678 bp in length
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                  Submitted (08-JUN-2001) DOE Joint Genome Institute, 2800 | Drive, Walnut Creek, CA 94598, USA
On Jun 8, 2001 this sequence version replaced gi:13811891
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                 Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 9011)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                   TTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAAACTCTGAATTCACATAC
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/chromosome="5"
/clone="CTD-2340N2"
a 18129 c 18543 g 2
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Pred. No. 8e-254;
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                             AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGGCGACAAAGGTGACCTGGGGCCTCG
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Sequence 510
AX136588
AX136588.1
                                                                                                                                                                                                                                                                                                                                                 Secretory protein or membrane protein
Patent: EP 1067182-A 510 10-JAN-2001;
Helix Research Institute (JP)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                           Ota,T., Isogai,T., Nishikawa,T., Kawai,Y.,
Hayashi,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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/db_xref="taxon:9606"
201 c 218 g 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZymoGenetics, Inc. (US)
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1 (bases 1 to 1117)
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Mammalia; Eutheria; Rodentia;
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/protein_id="CAC16633.1"
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                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
111. .851
                                                                                                                          WLRMGNGALHGDHQRFSTFAGFLLFETK"
272 c 293 g 268 t
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                         40.6%;
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Patent W00063377
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Score 695.8; DB 6;
Pred. No. 3e-165;
0; Mismatches 132;
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Maeda; T., Abe, M., Kurisu, K., Jikko, A. and Molecular cloning and characterization of encoding a putative secretory protein and in skeletal development
J. Biol. Chem. 276 (5), 3628-3634 (2001)
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Direct Submission
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                                                                                                                                                                      al Similarity
448; Conser
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Patent: WO 0149728-A 49 12-JUL-2001;
Protegene Inc. (JP) ; SAGAMI CHEMICAL
LOCATION/Qualifiers
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Mammalla; Eutheria; Primates; Catarrhini;
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/db_xref="taxon:9606"
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Search completed: January 15,

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ALIGNMENTS

RESULT 1
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KEYWORDS
SOURCE COMMENT REFERENCE FEATURES JOURNAL MEDLINE TITLE ORGANISM AUTHORS Athersys, Inc. 3201 Carnegie Ave, (Tel: 216 431 9900 Fax: 216 361 9596 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 776)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001) RST5388 Athersys RAGE Library Homo BG186424 BG186424 1 GI:13708111 EST. Contact: Scott J. Cain Homo sapiens 21227151 numan. l: scain@athersys.com quality sequence stop: 498. Location/Qualifiers Cleveland, 776 bp 9 44115, mRNA linear EST 21-APR-sapiens cDNA, mRNA sequence. USA EST 21-APR-2001

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/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080" 43.9%; 0, Score 751.8; DB 12 Pred. No. 2.3e-174; Length 776; 1; 60 1087 360 300 727 967 480 907 420 847 240

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1 (bases 1 to 874)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,B., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001) Tel: 216 431 9900 Fax: 216 361 9596 Athersys, Inc. 3201 Carnegie Ave, BG186928.1 RST5905 Athersys RAGE Library Homo Email: scain@athersys.com High quality sequence stop: Contact: Scott J. Cain Similarity Conservative a /db_xref="taxon:9606"
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/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances." 1. .874 Location/Qualifiers /organism="Homo sapiens" 43.48; Cleveland, 0, Score 743.4; DB 12; Pred. No. 2.8e-172; 0; Mismatches 41; 874 bp Э 44115, USP sapiens mRNA cDNA, mRNA sequence linear Length EST 4; Gaps 440 620 Ψ

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                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12807 row: f column: 13
                                                                                                                                                                                                                                                                                     Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 1103)
                                                                                                                                                                                                                                           Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/:
National Institutes of Health, N
                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                          quality sequence stop: 564.
Location/Qualifiers
                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5760396"
/clone=lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORTG; Site_1: NotI; Site_2: EcoRV (destroyed); source annonymous pool of 3 colons, age 26 yo male, 49 female, 71 yo male colon; 46 yo male kidney, and pool stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site
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Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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quality sequence stop: 504.
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/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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/clone="IMAGE:4592701"
/clone=lib="NIH_MCC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); S' and
SiI (ggccqctcggcc); Site_2: SiI (ggccattatggcc); S' and
3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
                                                                                                                                                                                /db_xref="taxon:9606"
                                                                                                                                                                                               /organism="Homo sapiens"
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GCAGGATTCCTGCTCTTTGAAACTAAACTAAATATATGACTAGAATAGCTCCACTTTGGGG
                                                                                                                                                                          TGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGATGACCTT
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, M Unpublished (1999) 602464652F1 NIH_MGC_75 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo Plate: LLCM1331 row: h column: found through the I.M.A.G.E. http://image.llnl.gov Mammalia; Eutheria; 1 (bases 1 to 828) quality sequence stop: Location/Qualifiers sequence GI:13293708 g Consortium/LLNL at Mammalian 14 mRNA cDNA clone Gene linear EST 12-m lone IMAGE:4592701 Collection (MGC) (LLNL) can be

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BASE COUNT
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603029396F1 NIH_MGC_114
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          CAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGC
                                  GCGGGGGCAGCATGGCCCCAAAGGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCA 426
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                                                                                                                                                                                  GCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCAC
                                                            GATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTT
                                                                                    GCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCA
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High quality sequence stop: 812.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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1 (bases 1 to 815)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:519982"
/clone_lib="NIH_MGC_114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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RST22308 Atl
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Athersys, Inc.
3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
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Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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Location/Qualifiers
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/cell_line="HT1080"
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/db_xref="taxon:9606"
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Pred. No. 2.8e-149;
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JOURNAL MEDLINE COMMENT REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION VERSION TITLE BG204962 RST24381 Athersys F BG204962 BG204962.1 GI:1372 Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 773)

Harrington, J.J., Sherf, B. Program.

Cain, S., Terroria. Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of genome-expression
activation of genome-wide protein expression libraries using random activation of genome-wide protein expression Contact: Scott J. 21227151 GI:13726649 Cain 773 bp RAGE Library H Homo sapiens linear s cDNA, EST 21-APR-2001 mRNA sequence.

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Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athers
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/clone_lib="Athersys RAGE Library"
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                                                                           CTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: graeme@helix.nih.gov
plate: 17 row: a column: 10
Seq primer: M13RP1 reverse primer (ABI).
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BQ637986
BQ637986.1 GI:21762445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Vis. 8 (4),
Contact: Wistow G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            splicing of other retina-preferred gene transcripts
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Homo sapiens cDNA clone
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1 (bases 1 to 636)
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                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                             /note-"Organ: Eye; Vector: pSPORTI; Neural retina tissue /note-"Organ: Eye; Vector: pSPORTI; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORTI vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGARCGGGCCCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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/clone_lib="Human Retina
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                                                                                                                                                       Contact: Scott J. Ca
Athersys, Inc.
3201 Carnegie Ave, (
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athers)
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
1 (bases 1 to 770)
1 (bases 1, J.J., Sher
                                                                                                                                                                                                                                                                                   Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
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                                                                                                                               l: scain@athersys.com
quality sequence stop:
   Location/Qualifiers
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Athersys RAGE Library I
/note-"See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily
                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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SOURCE ORGANISM

BG183776.1 EST. human. Homo sapiens

VERSION KEYWORDS

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BG183776 RST2684 Athersys BG183776

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RESULT 11 BG183776/c

REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 818)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smitl, E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher

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               GTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA 1550
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High quality sequence stop: 530
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Scott J. Cain Athersys, Inc.
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/cell_line="HT1080"
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Contact: Kim YS
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Fax: +82-42-860-4409
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21C Frontier Korean EST Project 2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,
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/db_xref="raxon:9606"
/clone="S18N669761-17-A08"
/clone_lib="S18N669761"
/sex="F"
                                                                                                                                                                                                                                                                                                                                                                                /note-*organ: Stomach: Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of TA RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand course of the coll was the strand the day of the strand the strand the day of the strand the strand the day of the strand the stra
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AA527298
AA527298.1 GI
                                           CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1007 Std Error: 0.000
                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R.
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mRNA sequence. BG571867 BG571867.1 GI EST.

BG571867 //94 bp #602593213F1 NIH_MGC_79 Homo sapiens

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/tissue_type="colon"
/lab_host="DH10B"
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Plate: LLCM1575 row: j column: 04
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Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/
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/clone_lib="NH_MGC_79"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
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Contact: Douglas Welton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by
Washington University Genome Sequencing Center For information
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IM
consortium, for clone orders contact: info@image.llnl.gov
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Celiular Biology, 7 Divinity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI964101 555 bp mRNA linear EST 1 le64h09:y1 melton Normalized Human Islet 4 N4-HIS 1 Homo CDNA clone IMAGE:5671913 5' similar to SW:CERL_RAT P98087 CEREBELLIN-LIKE GLYCOPROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
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1 (bases 1 to 555)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library
                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:5671913"
                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                          /dev_stage="Adult"
                                                                                                                                                                                                                                                 /tissue_type="Islets
                                                                                                                                                                                                                                                                           /sex="Both"
                                                                                                                                                                                                                                                                                              /clone_lib="Melton Normalized Human
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                                                                                                                                                                                                                                                   of Langerhans"
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Blistain, A.,
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481
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                                                                                                                                                                                                                                               762
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Local Similarity 100.0%; P
hes 555; Conservative 0;
                 AAGTCATTTGCAAAG 1136
                                                                        ACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCCAGCATCTTTATCACTCTTTCC 1061
                                                                                                                         TGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACC
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a 109 c
                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make thislibrary."
555
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Search completed: January 15, 2003, 19:31:52 Job time: 2259 secs

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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
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Gapop 10.0 , Gapext 1.0
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 US-09-188-930-28
US-09-370-838-151
US-08-463-911-6
US-08-463-911-1
US-08-893-467A-1
US-08-893-467A-1
US-08-99-195-5
US-09-195-5
US-09-195-1
US-09-118-1
US-09-336-33-33-344-1
US-08-393-336-1
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(without alignments)
6325.670 Million cell updates/sec
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Sequence 28, Appl
Sequence 151, App
Sequence 151, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 1, Appli
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Sequence 10, Appli
Sequence 10, Appli
Sequence 217, Appl
Sequence 264, Appl
Sequence 267, Appli
Sequence 62, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 33, Appli
Sequence 1, Appli
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392 495	332 435	272 375	212 315	152 255	92 195	sqr	290, App 1 1, App 1 1, App 1 1, App 1 11, App 1 11, App 1 11, App 1 161, App 1 163, App 1 17, App 1 17, App 1 17, App 1 17, App 1 18, App 1 19, App 1 19, App 1	Appli Appli 2, App

2;

В

436 AAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAGCATGGCCCCCAAAGGAT 495

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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Anthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANTION: and Methods For Their Use
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEO ID NOS: 348
SOFTWARE: FASTSEQ for Windows Version 3.0
SEO ID NO 203
TYPE: DNA
ORGANISM: Rat
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Query Match 40. Best Local Similarity 82. Matches 819; Conservative
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RESULT 3 US-09-370-838-151 ; Sequence 151, Application ; Patent No. 6444425

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                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08463911 Patent No. 5869330 GENERAL INFORMATION:
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                         COUNTY: 12173

ZIP: 02173

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPOTER: PC-DOS/MS-DOS

COLORS #1.0,
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CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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                 ARE: PatentIn Release #1.0, Version #1.30 APPLICATION DATA:
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EXCLUSIVELY IN ADIPOCYTES
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US/08/463,911
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                                   NUMBER OF SEQ ID NOS: 47
SOFTWARE: FRStSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 4517
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                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
                                                                                                                                                                                                              APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                   EARLIER APPLICATION NUMBER: 60/056,983 EARLIER FILING DATE: 1997-08-26
                                                                                                                                                                                                FILE REFERENCE: 97-49
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                    557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1313 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 338
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50.48;
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US-08-392-367B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5691197
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 i.
MEDIUM TYPE: 720 Kb storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
ent No. 5691197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                       ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 CTGGTGAGAAGGGTGAGAAAGGAGATCCAGGTCTTATTGGTCCTAAGGGAGACATCGGTG 270
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                                                                                                                                                            COMPUTER: IBM PS/2, Model 3
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                           STREET: Live 700
                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                     CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fay, Sharpe, Be ADDRESSEE: Minnich & McKee
                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210;
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        NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An Insolated DNA Sequence For
                                                                                                                                                                                       2, Model 35 SX
DOS 5.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6063901
. TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08893467A Patent No. 6063901
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TELEX: (216) 980162
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1868 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Nucleotide-c
FILING CALLS
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
NAME: MINNICH, RICHARD J.
24,175
                                                                                                       OPERATING SYSTEM: DOS 5.0
SOFTWARE: WOR'D Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/E
                                                                                                                                                                                                        ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 in
MEDIUM TYPE: 720 Kb storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kangas, Maarit
TITLE OF INVENTION: An Ins
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 Superior Avenue STREET: Suite 700
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fay, Sharpe, Beall, ADDRESSEE: Minnich & McKee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCGAGGAGAGAGGGCAGCAAAGGTGACATAGGTCTCACTGGCCCCAAGGGGGAACATG 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGCCTCCAGGGACTTACGGGTGCACCAGGGAAGCAAGGAGCAACTGGTGCTCCAGGAC 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCGTGATGGAACCCCAGGTGTCCAAGGACCCCAGGGCCCACCAGGCAGCAAGGAGGG 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGGCCTCGAGGGGGAGCGGGGGCAGCATG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCACCAAGGGAGACAAAGGGGACCTAGGCCTTCCAGGAAA 926
                                                                                                                                                                                                                                                                                                               Ohio
                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tryggvason,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elomaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 5691197 relevant
                                                                                                                                                                                       IBM PS/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide-genomic No. 5691197 relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such a Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide Chain Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a Collagenous Domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No. 6063901el Macrophage Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An Insolated DNA Sequence For a
                                                                                                                                                                                         Model 35 SX
                                                                                                           US/08/893,467A
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                                                                                                                                                                                                                                 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 2.2e-11;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5869330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08463911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 1:
                                TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: :
                                                              ATTORNEY/AGENT INFORMATION:
NAME: Granahan; Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHIS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1868 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: TR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Scherer, APPLICANT: Lodish, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 CCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGGAGCGGGGGCATG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1868 base pairs TYPE: Nucleic acid STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: ~02173
                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCCCAAAGGAGAAGGGCTACCCGGGGATTCCACCAGA 420
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128; Conserv
                                                                                                                                                                                                                                                                                                                                                                             Lexington
                                                                                                                                                                                                                                                                                                                                                                                            E: Hamilton, Brook
1276 base pairs
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L: No. 6063901 relevant
No. 6063901 relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r, Philipp E.
Harvey F.
A NOVEL SERUM I
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                                                                                                                                                                                                       US/08/463,911
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                                                                                                   WHI95-05
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                                                                                                                                                                                                                                                                                                                                                                                                             Smith & Reynolds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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; LOCATION:
US-08-463-911-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-794-795-5
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application Patent No. 5916766
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Best Local Similarity
Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/794,795
                                                                                                                                                                                                                                                                                     APPLICANT: Elshourlagy, Nabil
APPLICANT: Adamou, John
APPLICANT: Gross, Mitchell
APPLICANT: Lysko, Paul
TITLE OF INVENTION: Human Macro Scavenger Rec
TITLE OF INVENTION: eptor
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
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                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 GCATCCCAGGACATCCTGGCCACAATGGCACACCAGGCCGTGATGGCAGAGATGGCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 ACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACT 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 GCTACCCGGGGATTCCACCAGAACT---TCAGATTGCATTCATGGCTTCTCTGGCAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 ACAAAGGTGACCTGGGGCCTCGAGGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                         COMPUTER:
                                                                                                                                                                                            CITY: King of Prussia
                                                                                                                                                                                                                 STREET:
                                                                    OPERATING SYSTEM:
FILING DATE:
                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTATGACGGCAGCACTGGCAAGTTCTACTGCAACATTCCGGGACTCTACTACTTCTCTT
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                                                                                                                                              19406
                                                                                                                                                                              PA
                                                                                                                                                                                                                   709 Swedeland
                                                                                                                                                             USA
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                                                                                     IBM Compatible
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                                                                                                                                                                                                                   Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 231;
                                                     2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1276;
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US-09-249-200-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09249200 Patent No. 6197931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/7
FILING DATE: 04-FEB-1997
                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LYSKO, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ADAMOU, JOHN
APPLICANT: GROSS, MITCHELL
APPLICANT: LYSKO, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: ATGS(FILING DATE: 22-MAY-1996 ATTORNEY/AGENT INFORMATION: NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                726 AACTGGAACTAAGGGAGAGAAGGAGACCTGGGTCTCCCA 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 AGGAGCCAAAGGTGAGAAGGGCGACAAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              606 AGAGGCGGGCCTCCAAGGACCCCCAGGGTGCTCCAGGGAAGCAAGGAGCCACTGGCACCCC 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 TATGGGACGAGATGGAGCAACAGGCCCCTCGGGACCCCAAGGCCCCACCGGGAGTCAAGGG 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 GCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCA 415
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                                                                                                                                                                                                                                                                                    STREET: P.O. BUA CONTY: Valley Forge
                                                                          CLASSIFICATION:
                                                                                            APPLICATION NUMBER: US/09/249,200 FILING DATE: 12-FEB-1999
                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 610-270-4026
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                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGACCCCAAGGAGAAGGGCAAAGGCGATGGGGGTCTCATTGGCCCCAAAAGGGGGA
                                                                                                                                                                                                                                              19482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                   Ratner & Prestia
O. Box 980
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56.8%;
                                                                                                                                                                                                                                                                                                                                                                                          HUMAN MARCO SCAVENGER RECEPTOR
                                    08/794,795
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   60/017,699
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Pred. No. 5.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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US-08-794-795-1
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; MOLECULE TYPE:
US-09-249-200-5
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Best Local Similarity 56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICATE: 22-ma. -
FILING DATE: 22-ma. -
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
44
                                                APPLICATION NUMBER: US/08/794, FILING DATE: 04-FEB-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: ATG50009P FILING DATE: 22-MAY-1996
                                                                                                                                                                                                                                                        ZIP: 19406
COMPUTER READABLE FORM:
                                                                                                                                                               CURRENT APPLICATION DATA:
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LENGTH: 1560 base pairs
TYPE: nucleic acid
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TELEFAX: bit
Tex: 846169
                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 19406
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                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                             STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125;
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                                                                                                                                                                                                                                                                                              USA
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Lysko, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                     SmithKline Beecham Corporation
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Pred. No. 5.
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DB 4; 5.2e-10; 95;

Length 1560 Indels

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US-09-249-200-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: AT TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 12-FEB-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ELSHOURBAGY, NABI
APPLICANT: ADAMOU, JOHN
APPLICANT: GROSS, MITCHELL
APPLICANT: LYSKO, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                  TELECOMMUNICATION INFORMATION:
                                                                                 FILING DATE: 23-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       641
                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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                              NAME: Prestia, Paul F
REGISTRATION NUMBER: 23
REFERENCE/DOCKET NUMBER:
                                                                                                                                APPLICATION NUMBER: 08/7
FILING DATE: 04-FEB-1997
                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                           COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                     APPLICATION NUMBER: 60/017,699 FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Similarity 56.4%;
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FastSEQ for Windows Version 2.0
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610-407-0700
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                                                                                                                                                       08/794,795
                                              23,031
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Pred. No. 1.6e-09;
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; OTHER INFORMATION: Degenerate nucleotide sequence encoding the zsig39; OTHER INFORMATION: polypeptide of SEQ ID NO:2. US-09-140-804-10
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US-09-140-804-10
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SEQ ID NO 10
LENGTH: 729
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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Patent No. 6197930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REPERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER: OF SEQ. ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 TAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGG 255
                                                                                                                                                                                                        112 CCNGGNCAYCAYGGNWSNCARGGNYTNCCNGGNMGNGAYGGNMGNGAYGGNMGNGAYGGN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376
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  404
                                                                                                                         172
                                                                                                                                                               284 AACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAA 343
                                                                                                                                                                                                                                                224 CGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGA 283
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TELEX: 846169
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                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGACCCCAAGGAGAAGGGCAAAGGCGATGGGGGTCTCATTGGCCCAAAAGGGGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCA 375
CCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGC
                                                                              GGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAAGGGCTAC
                                                                                                                         GCNCCNGGNGCNCCNGGNGARAARGGNGARGGNGGNMGNCCNGGNYTNCCNGGNCCNMGN 231
                                          GGNGAYCCNGGNCCNMGNGGNGARGCNGGNCCNGCNGGNCCNACNGGNCCNGCNGGNGAR 291
                                                                                                                                                                                                                                                                                        164;
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28.2%; Pred. No. 6.7e-09;
7ative 72; Mismatches 343;
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Pred. No. 1.6e-09;
D; Mismatches 96;
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; TYPE: DNA
; ORGANISM: Rat
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US-09-188-930-19
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Best Local Similarity 56.0%;
Matches 117; Conservative
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SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 750
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
    567
                    387 AAGGAGAAGGGCTACCCGGGGATTCCA 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    644 TTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 AATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGAT 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 TGYWSNGTNCCNCCNMGNWSNGCNTTYWSNGCNAARWGNWSNGARWSNMGNGTNCCNCCN
                                                                                                                                                                                    TTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAG 326
                                                                                                          GTGAGAAGGGCGACAAAGGTGACCTGGGGCCCTCGAGGGGAGCGGGGGCAGCATGGCCCCA 386
                                                                       GACCCAAGGGGGTCAGTGGTACCCCCGGGAAACATGGTATACCGGGCAAGAAGGGACCTA
                                                                                                                                                   ACCGAGGAAAACAAGGACCAAAAGGGCAAAGCTGGGGGCCATTGGGAGAGCGGGTCCTCGAG
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AGGGCAAGAAAGGGGAACCTGGGCTCCCA 595
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                                                                                                                                                                                                                                                                                                         Score 61.8; DB 3; Length 750;
Pred. No. 2.3e-08;
0; Mismatches 92; Indels
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Search completed: January 15, Job time: 100 secs
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US-09-188-930-217
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 117; Conserv
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SEQ ID NO 217
LENGTH: 1107
TYPE: DNA
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APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 348
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                                                                     559
                                                                                                       387
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                                                                                                                                                                                                                                     267 TTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAG 326
                                                                                                                                                                                                                                                                                  379 ACGGCCAGGACGGAGACCGAGGGGACAGTGGAGAAGAAGGTCCACCTGGCAGGACAGGCA 438
                                                                                                                                                                                                                                                                                                                      207 ATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCA 266
                                                                                                       AAGGAGAGAGGGCTACCCGGGGATTCCA 415
                                                                                                                                       GACCCAAGGGGGTCAGTGGTACCCCCGGGAAACATGGTATACCGGGCAAGAAGGGACCTA 558
                                                                                                                                                             GTGAGAAGGGCGACAAAGGTGACCTGGGGGCCTCGAGGGGGAGCGGGGGCAGCATGGCCCCA 386
                                                                   AGGGCAAGAAAGGGGAACCTGGGCTCCCA
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5. 6150502
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               2003, 19:33:31
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Pred. No. 2.9e-08;
0; Mismatches 92;
                                                                   587
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Scoring table:
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Perfect score:
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Maximum DB seq length: 2000000000
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1367
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1: /SIDS2/gcgdata/
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1098	Result No.
1367 1367 1367 1367 1320.5 1320.5 1311 1208 884 792.5	
100.0 100.0 100.0 96.6 95.9 88.4 58.7	% Query Match
	Length DB
21 22 23 23 21 21 22 22 22 22	21 E
AAB18009 AAB88447 AAU84371 AAU84370 AAB29582 AAM99925 AAM99925 AAM41860 AAE06589	ID AAB15548
A novel polypeptid Human membrane or Novel human secret Novel human secret Movel human secret Mouse zacrp2 prote Human polypeptide Human portein havi	Description Human immune syste

ALIGNMENTS

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RRESULT 1
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IID AAB1
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Anti-inflammatory; keratolytic; anti-HIV. anti-allergic; antianaemic; antiarteriosclerotic; antiasthmatic; antidiabetic; nephrotropic; cancer; antigout; dermatological; antithyroid; virucide; hepatotropic; antibody; immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial; gene therapy; diagnostic; immunological disorder; viral infection; bacterial infection; fungal infection; parasitic infection; immunogen

Homo sapiens.

WO200060080-A2

12-OCT-2000.

04-APR-2000; 2000WO-US09072

05-APR-1999; 05-MAY-1999; 99US-0127852. 99US-0132647.

(INCY-) INCYTE PHARM INC.

Yue H, Lal P, Tang YT, Baughn MR, Azimzai Y, Lu DAM;

WPI; 2000-665005/64.

N-PSDB; AAA95787

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by the cDNA isolated as clone 1890540 from the Incyte BLADTUT07 library The human IMOLS (AAB15536-B15550) and their encoding polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 85; 95pp; English
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Human zacrp3; adipocyte complement related protein homologue
                                   Human adipocyte complement related protein homologue zacrp3, SEQ ID
                                                                           19-FEB-2001
                                                                                                                                                      AAB29580 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human immune system molecules 1-15 and polynucleotides encoding them useful for diagnosing, treating or preventing e.g. immunological disorders, infections, cell proliferative disorders, microbial
                                                                                                                                                                                                                                                                                      241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
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                                                                                                                                                                                                                                                     LLFETK 246
                                                                                                                                                                                                                                                                                    LLFETK 246
                                                                                                                                                                                                                                                                                                                                                                YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a human immune system molecule (IMOL) encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
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Pred. No. 2e-124;
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YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF

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MASLATHESNONSGIIFSSVETNIGNFFDVMTGREGAPVSGVYFFTFSMMKHEDVEEVYV

PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF

MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV

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                                                                                                                            Matches 246;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       anorexia, and conditions associated with these disorders. Due to its Clq like domain, zacrp3 and zacrp3-containing fusion proteins may be useful as antimicrobial agents, promoting lysis or phagocytosis of infectious organisms such as bacteria or viruses. Zacrp3, its fragments, fusion proteins, antibodies and activity modulators may also be used to inhibit collagen-induced platelet aggregation, adhesion, or activation, and may therefore have potential for promoting blood flow within the vasculature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the human zacrp3 protein (AAB29580) and to nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue of adipocyte complement related protein (ACRP30) and contains a collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a c-terminal Clq domain comprising 10 beta-strands. The zacrp3 gene is located on chromosome 5p12. The invention also relates to zacrp3 fragments, fusion proteins containing zacrp3 polypeptides, zacrp3-specific antibodies, expression constructs and host cells comprising zacrp3 nucleic acids, and methods of recombinant production of zacrp3. Human zacrp3, and its agonists and antagonists may be used in the study and modulation of cellular metabolism and energy balance in mammals, and may therefore be used to treat disorders such as obesity and mammals, and may therefore be used to treat disorders such as obesity and mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cellular metabolism; metabolic disorder; obesity; anorexia; antimicrobial agent; infection; platelet aggregation inhibition; adhesion; activation; vascular injury; antibacterial; antiviral.
                                                                                                                                                                                                                                                                                                  of a mammal e.g., to treat injury to the vasculature or other collagenous tissue. Human zacrp3 and its antibodies may additionally be used to study
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 109-110; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel zacrp3 polypeptides used to treat or prevent bacterial infections, for wound healing, improving blood flow, and to a energy efficiency in mammals .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piddington CS,
                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                           dimerisation and oligomerisation. The present sequence represents human
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                                                                1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
                                        MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120
                                                                                                                                                                                                               246 AA;
                                                                                                                            Conservative
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                                                                                                                                              100.0%;
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                                                                                                                                                 Score 1367; DB 2
Pred. No. 2e-124;
                                                                                                                            Mismatches
                                                                                                                                                                     21;
                                                                                                                            0
                                                                                                                                                                  Length 246;
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23-MAR-1999;
23-MAR-1999;
24-MAR-1999;
31-MAR-1999;
05-APR-1999;
21-APR-1999;
27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122; PRO189; PRO1890; PRO1887; PRO1785; PRO4357; PRO4357; PRO4405; PRO450; PRO4354; PRO4408; PRO5737; PRO4405; PRO5990; PRO640424; PRO4424; PRO44304; PRO4408; PRO5737; PRO4425; PRO5990; PRO6415; PRO4424; PRO4422; PRO44304; PRO4499; tumour; obesity; diabetes; insullnemia; kidney disorder; Bergers disease; nephropathy; Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      Crohns disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel polypeptide designated PRO1484.
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                                                                                                                                         Domain
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                                                                 2000WO-US05601.
                 99US-0125778.
99US-0125826.
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99US-0127706.
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                                                                                                                                                                                                              The present sequence represents a secreted or transmembrane polypeptide. CC The specification describes polypeptides designated PRO1484, PRO4334, CC PRO1122, PRO1889, PRO1889, PRO1887, PRO4785, PRO4355, PRO4355, PRO4356, PRO4356, PRO4350, PRO4350, PRO4356, PRO4356, PRO4350, PRO4424, PRO4408, PRO5737, PRO4405, PRO5737, PRO4405, PRO5737, PRO4405, PRO5737, PRO4405, PRO5737, PRO4405, PRO5900, CC PRO6030, PRO4424, PRO4402, PRO4409 and PRO4409. PRO1889 polypeptide is CC useful for diagnosing tumour in amammal. The polypeptides, their CC expression or activity of the polypeptide. Conditions treated include CC expression or activity of the polypeptide. Conditions treated include CC expression or activity of the polypeptide. The polypeptides are CC capable of inducing proliferation of mammalian kidney mesangial cells and are therefore useful for treating kidney disorders associated with CC decreased mesangial cell function such as Bergers disease or other CC mephropathies associated with Schonlein-Henoch purpura, cellac disease, CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used to generate transgenic animals for use in development and screening of CC therapeutically useful reagents and also for chromosome identification and tissue typing.
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 APR 1999
27 APR 1999
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03 AUG 1999
09 DEC 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel secreted and transmembrane polypeptides useful for diagnosing tumour in a mammal, for identifying agonists and antagonists of the polypeptide and for therapeutic use \,
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desnoyers L,
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
                                          Local Similarity
100.0%; Score 1367; DB 21; ilarity 100.0%; Pred. No. 2e-124; Conservative 0; Mismatches 0;
                                                                                                                                                       246 AA;
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, Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski PJ,
2hang Z;
                                                                         Length
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                                                                                 246;
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                                                                      PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                    protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAB88317 - AAF824295 and AAAF62232 - AAF62235 which are used to isolate to CDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HELI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human membrane or secretory protein clone PSEC0232.
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                                                                                                                                                      Local Similarity
              PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF
                                                                                    MLWRQLIXWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to nucleic acid sequences AAF93744 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-093989/11
                                                                  MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
PPG I PGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID 262; 609pp + CD ROM; English.
                                                                                                                                                                                                         246
                                                                                                                                      Conservative
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2000JP-0183766
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Pred. No. 2e-124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF62235 which are used to isolate the
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RESULT 5
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                                                                                 ameliorating various diseases such as inflammatory disorders (e.g. asthma), neurological disorders (e.g. dementia), haematopoletic disorders, skeletal developmental disorders, growth abnormalities, neurodegenerative disorders (e.g. Huntington's disease), nervous system disorders, autoimmune disorders (e.g. rheumatoid arthritis), peripheral myelinopathies, viral and bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disorder; neurological disorder; haematopoietic disorder; skeletal developmental disorder; growth abnormality; autoimmune disorder; neurodegenerative disorder; neurous system disorder; bacterial infection; peripheral myelinopathy; viral infection; cancer; obesity; diabetes; hypotension; sexual development disorder; blood disorder
                                                                                                                                                                                                                                                                                 Novel secreted and membrane-associated polypeptides and polynucleotides encoding the polypeptides, for preventing, treating and ameliorating cancers, mental or sexual developmental disorders, and malignant tumour.
                                                                                                                                                                           or membrane-associated proteins and the genes encoding them. The sequences of the invention are useful for treating, preventing and
                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABK35591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2000;
21-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SMITHKLINE BEECHAM CORP
SMITHKLINE BEECHAM PLC.
GLAXO GROUP LTD.
                                                                                                                                                                                                                                     Page 131-132; 151pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                          Cogswell JP,
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2000US-226517P.
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or sexual development disorders, and dysfunctions of the blood cascad system including those leading to stroke. AAU84362-AAU84389 represent the novel human secreted or membrane-associated proteins of the hypotension, obesity, bulimia, anorexia, manic depression, delirium, mental retardation, Tourette's syndrome, schizophrenia, growth, ment or sexual development disorders, and dysfunctions of the blood casca

growth, mental e blood cascade

alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; membrane-associated protein; hypertension; inflammatory disorder; neurological disorder; haematopoietic disorder; skeletal developmental disorder; growth abnormality; autoimmune disorder; neurodegenerative disorder; nervous system disorder; bacterial infection; peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
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                                                                          Novel secreted and membrane-associated polypeptides and polynucleotides encoding the polypeptides, for preventing, treating and ameliorating cancers, mental or sexual developmental disorders, and malignant tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypotension; sexual development disorder; blood disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted or membrane-associated protein #9.
                                                                                                                                                                                                                                                                                 Agarwal P,
                                                                                                                                                                                                                                                                                                                                    (GLAX
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                                                                                                                                                                                                                                                                                                                                                            SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                                                                                                                 Cogswell JP,
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Pred. No. 2e-124;
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                                                                                                                                                                                                                                                                                   Martensen
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Claim 1;

Page 130-131; 151pp; English

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RESULT 7
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma), neurological disorders (e.g. dementia), haematopoietic disorders, skeletal developmental disorders, growth abnormalities, neurodegenerative disorders (e.g. Huntington's disease), nervous s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human sor membrane-associated proteins and the genes encoding them. The sequences of the invention are useful for treating, preventing ameliorating various diseases such as inflammatory disorders (e)
                                                                                                                                                                                                                                                                          Mouse zacrp2; adipocyte complement related protein homologue; ACRP30; Clq domain; collagen-like domain; energy balance modulat cellular metabolism; metabolic disorder; obesity; anorexia; antimicrobial agent; infection; platelet aggregation inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                          WO200063377-A1
                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                               adhesion; activation; vascular injury; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse zacrp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention
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77.18;
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Pred. No. 9.3e-120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the human zacrp3 protein (AAB29580) and to concleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue cof adipocyte complement related protein (ACRP30) and contains a ccollagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-For repeats, and a ccollagen-like domain comprising 10 beta-strands. The zacrp3 gene is ccollagents fusion proteins containing zacrp3 polypeptides.

CC cacrp3-specific antibodies, expression constructs and host cells cc comprising zacrp3 nucleic acids, and methods of recombinant production of cc zacrp3. Human zacrp3, and its agonists and antagonists may be used in the cc study and modulation of cellular metabolism and energy balance in cc mammals, and conditions associated with these disorders such as obesity and anorexia, and conditions associated with these disorders may be useful cc as antimicrobial agents, promoting lysis or phagocytosis of infectious corganisms such as bacteria or viruses. Zacrp3, its fragments, fusion cc largen. Induced platelet aggregation, adhesion, or activation, and may coff and may coff and may coff and the collagen-induced platelet aggregation, adhesion, or activation, and may coff and may coff and the collagen.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          of a mammal e.g., to treat injury to the vasculature or other collagenous tissue. Human zacrp3 and its antibodies may additionally be used to study dimerisation and oligomerisation. The present sequence represents mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel zacrp3 polypeptides used to treat or prevent bacterial or viral infections, for wound healing, improving blood flow, and to analyze energy efficiency in mammals .
           AAM99925;
                                   AAM99925 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  zacrp2, a homologue of human zacrp3.
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                                                                                                                                                                                                                                                                                                   MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMKHEDVEEVYV 180
                                                                                                                                                                                                                                                 PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120
                                                                                                                        LLFETK 246
                                                                                                                                                2000-665243/64.
                                                                                                                                                                                                                                                                                                                                                        236;
                                                                                                                                                                                                                                                                                                                                                                                                         246 AA;
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9905-0294943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bishop PD
                                                                                                                                                                                                                                                                                                                                                                    95.9%;
                                   225 AA
                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                      Score 1311; DB 21; Pred. No. 5.5e-119; 2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                             Length 246;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                       0;
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08-SEP-2000; 08-SEP-2000;

2000US-0231968. 2000US-0232397. 2000US-0232398.

2000US-0232080.

2000US-0232081. 2000US-0231414. 2000US-0231413 08-SEP-2000; 08-SEP-2000; 06-SEP-2000; 06-SEP-2000; 05-SEP-2000; 05-SEP-2000;

2000US-0230437 2000US-0230438

2000US-0229513 2000US-0229509 2000US-0229345

2000US-0231242

2000US-0229343 2000US-0229344

2000US-0229287 2000US-0228924 2000US-0226868 2000US-0226681 2000US-0226279 2000US-0225759 2000US-0225758 2000US-0225757 2000US-0225447 2000US-0225270

000US-0227009

08-SEP-2000;

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; vulnerary; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-2002 (first entry)
Homo sapiens.
                                                                                  neurological disease; infection; human; secreted protein
                                                                                                                                                                                                                                                                                                                                         41
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17-JAN-2001; 2001WO-US01356

07-JUN-2000;

14-JUL-2000;

2000US-0218290

2000US-0225267 2000US-0225268

2000US-0225266 2000US-0225214 2000US-0224518

000US-0220964

2000US-0216880. 2000US-0217487. 2000US-0217496.

2000US-0216647 2000US-0214886 2000US-0209467 2000US-0205515 2000US-0198123 2000US-0189874 2000US-0186350 2000US-0184664 2000US-0180628 2000US-0179065

2000US-0232400. 2000US-0232401. 2000US-0233063.

25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

2000US-0235836 2000US-0235484 2000US-0234998 2000US-0234997 2000US-0234274 2000US-0233064 2000US-0233065

2000US-0236368 2000US-0236367 2000US-0236327

2000US-0236370 2000US-0236369

2000US-0237038

2000US-0239937 2000US-0239935 2000US-0237039

000US-0240960

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RESULT 9
AAM41860
ID AAM4
XX
AC AAM4
XX
DT 22-C
XX
DE Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                      cc and the encoded proteins (AAM9915-AAM9934) which are useful for cor gene therapy. The genes are isolated from a range of human tissues co disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention cof: (a) cancer, e.g. breast and ovarian cancer and other cancers of the cadrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, clung, or urogenital; (b) immune disorders e.g. Addison's disease, clailergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, codiabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid carthritis and ulcerative colitis; (c) cardiovascular disorders such as coveral, bacterial, fungal and parasitic infectious diseases such as coveral, bacterial, fungal and parasitic infections.

Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly covered.
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Sim
Matches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel human polynucleotides (AAI99513-AAI99538) and the encoded proteins (AAM99915-AAM99934) which are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids and polypeptides, useful for treating, preventing ameliorating human disorders and diseases \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAI99523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA,
            Human polypeptide SEQ ID NO 6791.
                                     22-OCT-2001 (first entry)
                                                               AAM41860;
                                                                                       AAM41860 standard; Protein; 202 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME
                                                                                                                                                        187
                                                                                                                                                                                208
                                                                                                                                                                                                          127
                                                                                                                                                                                                                                  148
                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                            2001-451924/48
                                                                                                                                                     11; SEQ ID NO 41; 465pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                    225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0251479
2000US-0251856
2000US-0251869
2000US-0251869
2000US-0251989
2000US-0251990
2000US-0251990
2000US-0251990
2000US-0254097
2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCI INC
                                                                                                                                                                                                                                                                                                                                                                            88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben
                                                                                                                                                                                                                                                                                                                                                                Score 1208; DB 22;
Pred. No. 4.9e-109;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MS
                                                                                                                                                                                                                                                                                                                                                                                          Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                66
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                                                                                                                                                                                                            186
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20-OCT 2000; 20-OCT 2000; 20-OCT 2000; 01-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000;

2000US-0246475

2000US-0246478 2000US-0246476 2000US-0246474 0000S-0244617

2000US-0241809 2000US-0241826

-0241808

08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000;

8 8

-NOV-2000

2000US-0246532 2000US-0246527

17-NOV-2000; 17-NOV-2000;

2000US-0249208. 2000US-0249209. 2000US-0249210. 2000US-0249211.

2000US-0249207 2000US-0246610 2000US-0246611 2000US-0246609 2000US-0246528 2000us-0246526

2000US-0246613

17-NOV-2000; 17-NOV-2000;

2000US-0249214

NOV-2000; NOV-2000;

17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 01-DEC-2000 01-DEC-2000 05-DEC-2000 05-DEC-2000

2000US-0249299. 2000US-0249300. 2000US-0250160. 2000US-0250391.

17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

2000US-0249218. 2000US-0249244. 2000US-0249245.

2000US-0249217 2000US-0249216 2000US-0249215 2000US-0249213 2000US-0249212

2000US-0249264. 2000US-0249265.

2000US-0249297

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Query Match
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                        C.N.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 6791; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-442253/47.
N-PSDB; AAI61016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                   specification.
                                                                                                                                                                                                                                                                                                                                                                                                      assays for receptor activity, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic;
     121
                                                                                                                   116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia.
                                                                               61
                                                                                                                                                                                             77
                                                                                                                                                                                                                                                   Local
                                                                                                                                                         _
                                                                         FTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN 180
                                                                                                                                                   FTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN 224
                                                                                                                                                                                           TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPE-----
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                                                                                                                                                                                                                                   al Similarity
170; Conser
                                                                                                                                                                                                                                                                                                                                                                    The sequence
                                                                                                                                                                                                                                                                                                                                                                                    disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                             202 AA;
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0598042.
2000US-0620312.
2000US-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0488725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressant; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                    data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodrich R,
                                                                                                                                                                                                                                                   64.7%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, useful for treating disorders system injuries -
                                                                                                                                                                                                                                                                                                                                                                    for this
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                                                                                                                                                                                                                                                 Score 884; DB 22;
Pred. No. 1.2e-77;
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Drmanac R
                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                patent did
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Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RT;
                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                    and therapy, drug screening, inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F,
                                                                                                                                                                                                                                                                     202;
                                                                                                                                                                                                                               32;
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                         115
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fertility), to modulate chemotactic and chemokinetic activity, modulate haemostatic and thrombolytic activity, to modulate re

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receptor б growth

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RESULT 10
AAE06589
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                                                                        CC mplo781. The polynuclectide and polypeptide of the invention (CC may be used in the prevention, diagnosis and treatment of diseases (CC associated with inappropriate polypeptide expression. The polynucleotides (CC into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA (CC polynucleotides and its complementary sequences may also be used as DNA (CC polypeptides may also be used as antipens in the production of antibodies (CC and in assays to identify modulators of polypeptide expression and (CC activity. The polypeptides and nucleic acids may be used as nutritional (CC supplements, to modulate cytokine and cell proliferation activity, to (CC modulate immune stimulation or suppression (e.g. for the treatment of medulate insulation and insulin-dependent diabetes), to modulate (CC contents), to modulate insulation activity (e.g. for the controlling (c.g. for the controlling contents), to modulate activin and insulin-dependent diabetes), to modulate activin and insulin-dependent diabetes), to modulate activin and insulin activity (e.g. for controlling controll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, \, Alzheimer's and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; haematopoiesis; tissue growth activity; Parkinson's chemokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 308-309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2000;
03-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein having hydrophobic domain, HP10781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200149728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE06589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE06589 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence is human protein with hydrophobic domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALHGDHQRFSTFAGFLLFETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALHGDHQRFSTFAGFLLFETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-418355/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hydrophobic domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD12584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGAMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000JP-0000585.
; 2000JP-0000588.
; 2000JP-0002299.
; 2000JP-0026862.
; 2000JP-0058367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-JP09359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinfertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             563pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disorder; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nutritional supplement;
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Sequence

223

AA;

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Matches
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AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY11374 to AAY11331, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, hammatopoics is regulating activity, tissue growth regulating activity, haemostatic and regulating activity, chemostatic activity, haemostatic and
                                                                                                                                                                                  New nucleic acids encoding human secreted cDNA libraries prepared from substantia ni and fetal brain tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therap; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                      Claim 34; Page 402-403; 434pp; English.
                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human 5' EST secreted protein SEQ ID No 307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY11485 standard; Protein; 128
                                                                                                                                                                                                                                                         WPI; 1999-153781/13.
                                                                                                                                                                                                                                                                                   Duclert A, Dumas Milne Edwards J, Lacroix B;
                                                                                                                                                                                                                                                                                                                                         01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                  11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              WO9906551-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          НОПО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombolytic;
                                                                                                                                                                                                                                                                                                               (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                      31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYPGIPPELQIAFMASLATHFSNQNSGIIFSSYETNIGNF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHPKTGTVDNNTSTDLKSLRPDELPHPEVDDLAQITTFWGQSPQTGGLPPDCSKCCHGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFRGYQGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
147; Conserv
                                                                                                                                                                                                                                           AAX39551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                           97US-0905133
                                                                                                                                                                                                                                                                                                                                                                      98WO-IB01235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                 proteins obtained from ra, cerebellum, surrenals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 12
AAM40074
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                                                                                                                                                  09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                   Wang
                                                                                              Tang
                                                                                                                                                                                                                                                                                                                                          peripheral nervous system; neuropathy; central nervous system; CNS; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                         Zhao
                                                                                                                                                                                                          21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                           26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                 26-JUL-2001.
                                                                                                                                                                                                                                                                                       WO200153312-A1
                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                             Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM40074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM40074 standard; Protein; 126 AA
                                                                                                                                          29-NOV-2000;
                                                                                                                    (HYSE-)
                                                                                                                                                                                                                                                                                                                                  leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 MASL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120
                                       2001-442253/47.
DB; AAI59230.
                                                                        J, AQ
                                                                                                                                                                                                                                                                                                             sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124;
                                                                                                                                                                                                                                                                                                                                                                                      nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                   HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                       Liu C,
Wang z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 AA;
                                                                                                                                        2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative (
                                                                                                                                                                                                          2000US-0488725.
2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                 Asundi V, (
                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3219.
                                                                         Goodrich
                                                                                 Chen R,
Xu C,
                                                                         ¤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 721; DB 20;
; Pred. No. 4.2e-62;
0; Mismatches 0;
                                                                        nen R, Ma Y,
Ku C, Xue AJ,
Drmanac RT;
                                                                                   Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                    Zhang
                                                                                              Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                    Ċ,
                                                                                              Wang
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -

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RESULT 13
AAY75969
ID AAY75
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinjinhibin activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                   Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell secreted; transmembrane; inflammation; cancer; neurological disease;
                                                                                                                                                                                                                   WO9955865-A1
                                                                                                                                                                                                                                              Rattus sp
                                                                                                                                                                                                                                                                                         angiogenesis; tumour vascularisation; growth disorder;
developmental disorder; skin wound; hair follicle disorder;
                                                                                                                                                                                                                                                                                                                                                                               Rat skin cell protein, SEQ ID 147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY75969 standard; Protein; 105 AA
                           WPI; 2000-072177/06
                                                      Strachan L,
                                                                                                                                                           29-APR-1999;
                                                                                                                                                                                                                                                                          anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                   (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 MASLATHESNQNSGIIFSSVETNIGNEFDVMTGREGAPVSGVYFETESMMKHEDVEEVYV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lmmunosuppressant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic, unosuppressant and cytostatic activity. The polynucleotides are u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLFETK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLFETK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                       Sleeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IJ
                                                                                                               98US-0069726.
98US-0188930.
                                                                                                                                                           99WO-NZ00051.
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                                                                                                                                                                                                                                                                          cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3219; 10078pp; English
                                                       Watson JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 663;
Pred. No.
                                                                                                                                                                                                                                                                             neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                       Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                       Kumble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 126;
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                                                       P
                                                       Murison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                       JG
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Novel polynucleotides useful for

the

treatment of various

conditions

Novel polynucleotides useful for the treatment of various

conditions

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RESULT 14
AAY76025
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AAY75942-Y76123 represent polypeptides encoded by cDNA sequences derived from several mouse, rat or human skin cell types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and AAY76119 are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071, AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
                                                                                                                                                                                                                                                                                                                                               Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying c secreted; transmembrane; inflammation; cancer; neurological disea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 112-113; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel nucleic acid sequences derived from rat
                          WPI; 2000-072177/06.
N-PSDB; AAZ61730.
                                                                      Strachan L,
                                                                                                                                  29-APR-1998;
09-NOV-1998;
                                                                                                                                                                              29-APR-1999;
                                                                                                                                                                                                          04-NOV-1999
                                                                                                                                                                                                                                        WO9955865-A1
                                                                                                                                                                                                                                                                      Rattus sp.
                                                                                                                                                                                                                                                                                                   anti-inflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                 angiogenesis; tumour vascularisation; growth disorder;
developmental disorder; skin wound; hair follicle diso
                                                                                                                                                                                                                                                                                                                                                                                                            Rat skin cell protein, SEQ ID NO:280
                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY76025 standard; Protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         putative transmembrane domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               including wounds and cancer
                                                                                                   (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLRRQLVWWHLLALLFLPFCLCQDEYMESPQAGGLPPDCSKCCHGDYGFRGYQGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                        Sleeman
                                                                                                                               98US-0069726
98US-0188930
                                                                                                                                                                              99WO-NZ00051
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                                                                        Watson
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Pred. No. 1e-48;
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                                                                        Onrust
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                                                                                                                                                                                                                                                                                                                                               neurological disease;
                                                                        Kumble
                                                                                                                                                                                                                                                                                                                    disorder;
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                                                                        Murison
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                                                                                                                                                                                                                                                                                                                                                              cell;
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including wounds and cancer -

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RESULT 15
AAB55908
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation,
                                                                                                                                                                                                                                                                                                                                        keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
                                                                                                                                                                                                                                                    23-NOV-2000
                                                                                                                                                                                                                                                                                WO200069884-A2
                                                                                                                                                                                                                                                                                                               Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                            Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                            Skin cell protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB55908 standard; Protein; 105 AA
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           New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -
                                                                                                                       Watson JD,
                                                                                                                                                                                      14-MAY-1999;
                                                                                                                                                                                                                     15-MAY-2000; 2000WO-NZ00075.
                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKG 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLWROLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG 60
                                                                         2001-007495/01.
DB; AAC99566, AAC99776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLRRQLVWWHLLALLFLPFCLCQDEYMESPQAGGLPPDCSKCCHGDYGFRGYQGPPGPPG
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98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 AA;
                                                                                                                       Strachan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                      99US-0312283.
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
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Pred. No. 1e-48;
2; Mismatches
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                                                                                                                         Kumble KD,
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Best Local Similarity
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                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 147; 352pp; English.
                                                                                                                                                                                                                                                                    oligonucleotides for examining expression patterns.
 61
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                                     PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKG 105
                                                                         MLRRQLVWWHLLALLFLPFCLCQDEYMESPQAGGLPPDCSKCCHGDYGFRGYQGPPGPPG
                                                                                           MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKG 105
                                                                                                                                                     98;
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93.3%;
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Pred. No. 1e-48;
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Search completed: January 15, 2003, 19:37:10

Job time : 81 secs

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Maximum DB seq length: 2000000000
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1 MLWRQLIYWQLLALFFLPFC
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Maximum Match 100%
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US-09-336-536-20
US-09-140-804-8
US-09-118-408-3
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US-09-336-536-4
US-09-336-536-10
US-09-336-536-11
US-09-188-930-295
US-09-118-408-44
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Sequence 280, App
Sequence 294, App
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WESULT 2 US-09-188-930-280 Sequence 280, Application US/09188930A PAPLICANT: NETCHANTION: APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Strachan, Matthew APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene APPLICANT: Nurison, James Greg TITLE OF INVENTION: Compositions Isolated From Skin Cel	Qy 61 PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKG 10 	Query Match 42.6%; Score 582; DB 4; Lengt Best Local Similarity 93.3%; Pred. No. 2.1e-51; Matches 98; Conservative 2; Mismatches 5; Ind Qy 1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQAGGLPPDCSKCCHGDYS	RESULT 1 US-09-188 930-147 Sequence 147, Application US/09188930A Patent No. 615502 GENERAL INFORMATION: APPLICANT: Watson, James D. APPLICANT: Sleeman, Matthew APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene APPLICANT: Murison, James Greg TITLE OF INVENTION: Compositions Isolated From Skin Cel TITLE OF INVENTION: and Methods For Their Use FILE REFERENCE: 11000.1011c1 CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348 SOFTMARE: FastSEQ for Windows Version 3.0 SEQ ID NO 147 LENGTH: 105 TYPE: PRT ORGANISM: Rat US-09-188-930-147	. ALIGNMENTS	28 219 16.0 245 4 US-09-140-804-4 29 202 14.8 215 4 US-09-180-804-5 30 200.5 14.7 198 4 US-09-180-930-138 31 196 14.3 222 4 US-09-140-804-7 32 194 14.2 185 2 US-08-463-911-3 33 192 14.0 623 4 US-09-29-348-2 35 186 13.6 236 4 US-09-029-348-2 35 186 13.6 236 4 US-09-029-348-2 37 185 13.5 357 1 US-08-0475-041A-66 38 185 13.5 357 1 US-08-475-041A-66 39 185 13.5 357 4 US-08-475-01A-66 40 184.5 13.5 357 4 US-08-475-029A-66 40 184.5 13.5 684 1 US-08-55-669-12 41 184.5 13.5 684 3 US-08-794-796-7 42 183.5 13.4 489 2 US-08-794-796-7 43 183 13.4 489 4 US-08-392-367B-2
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FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A

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US-09-188-930-294
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 294
LENCTH: 294
TYPE: PRT
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NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 280
LENGTH: 105
TYPE: PRT
ORGANISM: Rat
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APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Watson, James D
                                                                                                                                                                      175 PIKEDKILMNEGGHYNASSGKFVCSVPGIYYFTYDITLANKH-----LAIGLVHNGQ--Y 227
                                                                                                                               191 SMYSYEMK-GKSDTSSNHAVLKLAKGDEVWLRM----GNGALHGDHQRFSTFAGFLLF 243
                                                                                                                                                                                                              134 GIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMM---KHEDVEEVYVYLMHNGNTVF 190
                                                                                                                                                                                                                                                     115 GPRGPKGVSGTPGKHGIPGKKGPKGKKGEPGLPGPCSCGSSRAKSAFSVAVTKSYPRERL 174
                                                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                                                                                                                                                  55 GPPGAPGSSGMVGRMGFPGKDGQDGQDGDRGDSGEEGPPGRTGNRGKQGPKGKAGAIGRA 114
                                                                                                                                                                                                                                                                                                                                                                            60 GPPGIPGNHGNNGATGHEGAKGEKGDKGD------ 92
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                                                                                               RIRTFDANTGNHDVASGSTILALKEGDEVWLQIFYSEQNGLFYDPYWTDSLFTGFLIY 285
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93.3%;
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US-09-530-423-2
; Sequence 2, Application US/09530423
; Patent No. 6461821
; GENERAL INFORMATION:
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               APPLICANT: Otsuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Smooth muscle growth in
TITLE OF INVENTION: diagnostic method for
TITLE OF INVENTION: therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5869330
FILE REFERENCE: P98-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Scherer, I APPLICANT: LOGISH, H TITLE OF INVENTION: I TITLE OF INVENTION: I NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                        116
                                                                                                                                                                                                                            227 LYADNVNDSTFTGFLLY 24:
                                                                                                                                                                                                                                                             227 LHGDHQRFSTFAGFLLF 243
                                                                                                                                                                                                                                                                                                   169 VY--MKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDHNG 226
                                                                                                                                                                                                                                                                                                                                         171 KHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRM-GNG---A 226
                                                                                                                                                                                                                                                                                                                                                                            109 EAAYMYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHIT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Mac
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les 81; Conserv
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 IPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGER---GQHGPKGEKGYPGIPPE----- 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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SYSTEM: PC-DOS/MS-DOS
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Harvey F.
A NOVEL SERUM PROTEIN PRODUCED
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US-09-530-423-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: JP I PRIOR FILING DATE: 1997-10-29
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CURRENT FILING DATE: 2000-05-01
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                                                                        TELEFAX: (617) 861-954 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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                                                                                                                                                      REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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  MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                      TOPOLOGY:
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                                                        LENGTH:
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Lodish, Harvey F.
VENTION: A NOVEL SERUM PROTEIN PRODUCED
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protein
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Pred. No. 7.6e-22;
5; Mismatches 78;
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US-09-336-536-20

US/09336536

Sequence 20, Application Patent No. 6406884 GENERAL INFORMATION:

APPLICANT: Leiby, K.
APPLICANT: MCKBY, C.
APPLICANT: MCKBY, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

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LENGTH: 2
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sheppard, Paul O. APPLICANT: Humes, Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 YDGSTGKFHCNIPGLYYFAYHITVY--MKDVKVSLFKKDKAMLFTYDQYQENNVDQASGS 200
201 VLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240
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                                 AVLKLAKGDEVWLRM-GNG---ALHGDHQRFSTFAGFLLF 243
                                                                           YDGSTGKFHCNIPGLYYFAYHITVY--MKDVKVSLFKKDKAMLFTYDQYQENNVDQASGS 200
                                                                                                                                                  TGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNH 142
                                                                                                                                                                                      RGQHGPKGEKGYPGI-----PPE----LQIAFMASLATHFSNQNSGIIFSSVETNIGNF 147
                                                                                                                                                                                                                            FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNH
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                                                                                                             FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNH 207
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Pred. No. 8.2e-22;
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US-09-336-536-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Otsuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Smooth muscle growth inhibitory composition,
TITLE OF INVENTION: diagnostic method for arteriosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09530423 Patent No. 6461821
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CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP H9-297569 PRIOR FILING DATE: 1997-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/530,423 CURRENT FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: 1
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                                        208 AVLKLAKGDEVWLRM-GNG---ALHGDHQRFSTFAGFLLF 243
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nes 76; Conserv
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VLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240
                                                                                  YDGSTGKFHCNIPGLYYFAYHITVY--MKDVKVSLFKKDKAMLFTYDQYQENNVDQASGS 200
                                                                                                                          FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNH
                                                                                                                                                                    TGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNH 142
                                                                                                                                                                                                             RGQHGPKGEKGYPGI-----PPE----LQIAFMASLATHFSNQNSGIIFSSVETNIGNF 147
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                                                                                                                                                                                                                                                                                                                                                           21.5%; Score 293.5; DB 4 34.5%; Pred. No. 8.2e-22;
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: SEQ ID NO 8
: LENGTH: 247
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-140-804-8
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                                                                                    ; ORGANISM: HOMO
US-09-118-408-3
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US-09-140-804-8
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                                                                                                                      SEQ ID NO 3
LENGTH: 247
TYPE: PRT
  Query Match
Best Local S
Matches 82
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Best Local Similarity
Matches 82; Conserv
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                        EARLIER FILING DATE: 1997-07-18 NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/053,154
                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/118,408A CURRENT FILING DATE: 1998-07-17
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Pred. No. 3.8e-21;
Score 287; DB 4; I
Pred. No. 3.8e-21;
0; Mismatches 101;
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6 LIYWQLLALFFLPFCLCQDEYMESPQTGG--LPPDCSKCCHGDYSFRGYQGPPGPPGPPG 63

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CURRENT APPLICATION NUMBER: US/09/506,855; CURRENT FILING DATE: 2000-02-17; NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 3; SEQ ID NO 3; LENGTH: 247; TYPE: PRT.; ORGANISM: Homo sapien
US-09-506-855-3
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US-09-506-855-3
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US-08-463-911-4
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APPLICANT: Sheppard, Paul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
TITLE OF INVENTION: IMMUNE FUNCTION
FILE REFERENCE: 99-12
                                      Sequence 4, Application US/08463911 Patent No. 5869330 GENERAL INFORMATION:
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Best Local Similarity
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                      APPLICANT:
    APPLICANT:
                                                                                                                                                                                                227 LHGDHQRFSTFAGFLLF 243
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                                                                                                                                                                                                                                                                                                                                                                                                                  49 HPGHNGTPGRDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPQTPGRKGEPG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                               64 IPGNHGNNGATGHEGAKGEKGDKGDLGPRGER----GQHGPKGEKGYP------GIPP 114
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Lodish, Harvey
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                  Scherer,
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NUMBER OF SEQ ID NOS:
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APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Mohamath, Roadoh

APPLICANT: Mohamath, Roadoh

APPLICANT: Mohamath, Roadoh

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF

TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.475C1

CURRENT APPLICATION UNMBER: US/09/370,838

CURRENT FILING DATE: 1999-08-09

EARLIER APPLICATION NUMBER: US 09/285,323

EARLIER FILING DATE: 1999-04-02
                                                                                                                                                                                                                                                                                                                            RESULT 14
US-09-370-838-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-463-911-4
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                       Sequence 185, Application US/09370838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 861-95.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                 19 NSKQVSSGGALLRLQRGDEVWLSVNDYNGMV-GIEGSNSVFSGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 GKSDTSSNHAVLKLAKGDEVWLRMG--NGALHGDHORFSTFAGFLLF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 YNPSTGKFTCEVPGLYYFVY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSM------YSYEMK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 GEKGYPGIP-----PELQ-----IAFMASLATHFSNQNSGIIFSSVETNIGNF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 GTSGLPGDPGPRGPPGEPGVEGRYKQKHQSVFTVTRQTTQYPEANALVRFNSVVTNPQGH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 GCYGIPGMPGMPGAPGKDGHDGLQGPKGEPGIPAVPGTQGPKGQKGEPGMPGHRGKNGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GYQGPPGPPGPPGIPGNHGNNGNNGATGH-----EGAKGEKGDKGDLGPRGERGQHGPK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/463,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 31.3 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617) 861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 274; DB 2; L
Pred. No. 7.6e-20;
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                                                                                                                       FOR THEIR USE
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CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 185 LENGTH: 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09336536
Patent No. 6406884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.0%;
Best Local Similarity 29.6%;
Matches 72; Conservative 4
                                                                                                                                                                                                                                                                                                          Query Match 19.38
Best Local Similarity 32.48
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-336-536-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Leiby, K.
APPLICANT: MCKay, C.
APPLICANT: BOSSONE, S.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 683 LMKNEEVLVSAYANDGAPDHETASNHAILQLFQGDQIWLRLHRGAIYGSSWKYSTFSGYL 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              623 RTSNLAPGTLDQPIVEDLLLNNLGETFDLQLGRENCPVNGTYVFIFHMLKLAVNVPLYVN 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        743 LYQ 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 LFE 244
189 QVWVQVGVGDYIGIYASIKTDSTFSGFLVY 218
                                                                                                        161 GVYFFTFSMMKHEDVEEVYVY--LMHNGNTVFSMYSYEMKG--KSDTSSNHAVLKLAKGD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 LATHES -- NONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        565 QVSSPE-RDNETFNSGDSGQGDSRSMTPVDVPVTNPAATILPVHVYP-LPQQMRVAFSAA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509 GLP----SISNGNYSQLQFQAREYSGAPYSQRDNFQQCYKRGGTSGGPRANSRAGWSDSS 564
                                      217 EVWLRMGNG----ALHGDHQRFSTFAGFLLF 243
                                                                            134 GVYYFAV----HATVYRASLQFDLVKNGESIASFFQF-FGGWPKPASLSGGAMVRLEPED 188
                                                                                                                                                                             101 HGPKGEKGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVS 160
                                                                                                                                                                                                                                34 GLPPDCSKCCHGDYS-----FRGYQGPP-------GPPGPPGIPGNHGNNGNN 74
                                                                                                                                                       74 AGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 GATGHEGAKGEKGDKGDLGPRGERGQ-----HGPKGE----KGYPGIPPELQIAFMAS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                              19.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 273; DB 4;
Pred. No. 4.4e-19;
                                                                                                                                                                                                                                                                                                            Score 264.5; DB 4; Length 228;
Pred. No. 6.3e-19;
6; Mismatches 79; Indels 27
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                                                                                                                                                                                                                                                                                                              27; Gaps
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Search completed: January 15, 2003, 19:41:37 Job time: 37 secs

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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
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2:
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prin and is derived by analysis of the total score distribution.
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ALIGNMENTS

RESULT 1 JC4708 JC4708 gelatin-binding 28K protein precursor - human N;Alternate names: adipose specific collagen-like factor C;Species: Homo sapiens (man) C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Sep-1999 C;Accession: JC4708; JC4944 R;Maeda, K; Okubo, K; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K. Biochem. Biophys. Res. Commun. 221, 286-289, 1996 A;Title: CDNA cloning and expression of a novel adipose specific collagen-like factor A;Peference number: JC4708; MUID:96224171; PMID:8619847 A;Accession: JC4708 A;Molecule type: mRNA A;Residues: 1-244 <maed- 1-244="" <maed-<="" a;residues:="" th=""></maed->
Alternate names: adipose specific collagen-like factor Species: Homo sapiens (man) Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Sep-1999 Accession: JC4708; JC4944 Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubacchem. Biophys. Res. Commun. 221, 286-289, 1996 Title: cDNA cloning and expression of a novel adipose specific collagen-likeference number: JC4708; MUID:96224171; PMID:8619847 Accession: JC4708 Molecule type: mRNA Residues: 1-244 «MAE»

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 104-112; /x', 114-117; 453-466 <NIN2>
A; Residues: 104-112; /x', 114-117; 453-466 <NIN2>
C; Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl
C; Keywords: coiled coil; extracellular matrix; glycoprotein; homotrir
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 1-18/Domain: complement Clq carboxyl-terminal homology <ClQ>
F; 453, 456/Modified site: hydroxyproline (Pro) #status experimental
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A;Residues: 'T',9,'D',11-12,'EDQMKLYILFTM',30-31,'TCKSGRAFTTYMILQNVWADLVSSHT',48-89,'L'
629, 'PQAVLSLISWRTIKCGSSCQIQNPMVSIPLNMFILLSQVSYLLKSNNIPLTMS' <NIN1>
A;Cross-references: EMBL:M13496; NID:g211699; PIDN:AAA48736.1; PID:g211700
A;Accession: S77711
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A;Residues: 1-674 <NIN>
R;LuValle, P; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
J. Biol. Chem. 263, 18378-18385, 1988
A;Title: The type X collagen gene. Intron sequences split the
A;Reference number: A31896; MUID:89054019; PMID:2461368 .
A;Accession: A31896
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C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C;Accession: S23297; A31896; S65594; S77711; I50218
R;Ninomiya, Y; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle,
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A;Residues: 1-75 <LUV>
R;Nionmiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsenmayer, T.; Olsen,
J. Biol. Chem. 261, 5041-5050, 1986
A;Title: The developmentally regulated type X collagen gene contains a long open
A;Reference number: I50218; MUID:86168227; PMID:3082876
A;Accession: S65594
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A; Accession: S23297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
                                                                                                        665
                                                                                                                                                                                                                                                                      179
                                                                                                                                                                                                                                                                                                                           547
                                                                                                                                                                                                                                                                                                                                                                                                                              487 PPGPKGNSGEPGLPGPPGPPGPPGQSTIPEGYVKGESRELSGMSFMKAGANQALTGMPVS 546
                                                                                                                                                           236 TFAGFL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHGPKGEKGYPGIP----
                                                                                                                                                                                                                WVALYKNGSPVMYTYDEYQKGYLDQASGSAVIDLMENDQVWLQLPNSESNGLYSSEYVHS 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240
                                                                                                        SESGEL 670
                                                                                                                                                                                                                                                                   YVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN---GALHGDHQRFS 235
                                                                                                                                                                                                                                                                                                                           AFTVILSKAYPGATVPIKFDKILYNRQQHYDPRTGIFTCRIPGLYYFSYHV--HAKGTNV 604
                                                                                                                                                                                                                                                                                                                                                                           AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type X collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.5%; Score 280.5; DB 2; 30.9%; Pred. No. 2.3e-15; tive 23; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -PELQI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chicker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carboxyl-terminal homology
; homotrimer; hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5'-untranslated region and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olsen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reading
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R
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                   δÃ
                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: Coll0a-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 'SDGYFSQ', 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-680 <KON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collagen alpha 1(X) chain precursor -
C; Species: Mus musculus (house mouse)
                                                                                                                                                                                    Matches
                100 QHGPKGEKGYPGIP--
                                                                                                                                                                                                                Local
                                                                                                                                                                                    1 Similarity
                                                                                                                                                                                    Conservative
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A; Molecule type: mRNA
A; A; Molecule type: Molecule
A; A; Molecule type: Molecule
A; A; Molecule
A; Biochem: 206, 217-224, 1992
A; Title: Cloning of the human and mouse type X collagen genes and mapping of the mous
A; Reference number: I48299; MOID:92267014; PMID:1587271
A; Accession: I48299
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: $2-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',
A;Residues: $52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',
A;Residues: $52-247,'L',249-285,'A',B019-280,'EAA46237.1; PID:g667031
A;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an ar
A;Reference number: $26397; MUID:88087150; PMID:2826450
A;Accession: $26397
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A;Title: Characterization of the mouse type X collagen gene A;Reference number: S30127; MUID:93261348; PMID:8492743
A;Accession: S30127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481 R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Biochim. Biophys. Acta 1130, 78-80, 1992 A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen A;Reference number: S22215; MUID:92182017; PMID:1543751 A;Accession: S22215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: collagen alpha l(VIII) chain; complement C1q carboxyl-terminal homolog C;Keyeords: coiled coil: extracellular matrix; glycoprotein; homotrimer F;1-18/Domain: signal sequence #status predicted <SIG> F;19-680/Product: collagen alpha l(X) chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 385-450,'K',452-627 <ELA>
A;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kong, R.Y.C.; Kwan, K.M.; Lau, E
Eur. J. Biochem. 213, 99-111, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830
R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-285, 'A', 287-680 <ELI>
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A;Accession: S31216
                                                                                                                                                                                                                                                                                                                                                                                                                                     :553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>
                                                                                   GEPGIPGTRGPTGPPGVPGFPGSKGDPGNPGAPGPAGIATKGLNGPTGPPGPPGPRGHSG 502
                                                                                                                                                                      GDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATG----HEGAKGEKGDKGDLGPRGERG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , 24-26, 'KQ' <SUM>
                                                                                                                                                                                                                                                                                                             20.4%;
                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                             Score 278.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                   Mismatches
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-- PELQ---
                                                                                                                                                                                                                                                                                                        3.4e-15;
                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                   Indels 45;
                                                                                                                                                                                                                                                                                                                                        Length 680;
-IAFMASLATHF 128
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                                                                                                                                                                                                                                                                   Gaps
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A; Reference number: S29328; MUID:93011118; PMID:1396691
A; Accession: S29328
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-246 < PET>
A; Cross-references: EMBL:X66295; NID:950228; PIDN:CAA46993.1; PID:950229
A; Cross-references: EMBL:X66295; NID:950228; PIDN:CAA46993.1; PID:950229
C; Superfamily: complement subcomponent C1q chain A; complement C1q carbox
F;122-245/Domain: complement C1q carboxyl-terminal homology <C10>
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C:Superfamily: C:Keywords: coi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999
C:Accession: S13301
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R:Petry, F.; Reid, K.B.M.; Loos,
Eur. J. Biochem. 209, 129-134, 1
                                                                                                                                                                                                                                                                                                                                          complement subcomponent C1g chain C - mouse
C; Species: Mus musculus (house mouse)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-674 < THO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 GHNGEAGPRGVPGIPGTRGPIGPPGIPGFPGSKGDVGTPGPPGPAGIAVKGLNGPTGPPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GYQGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGD------KGDLGPRGERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity les 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAYPAIGTPIPFDKILYNKQQHYDPRTGIFTCKIPGIYYFSYHI--HVKGTHAWVGLYKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRM---GNGALHGDHQRFSTFAGFLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTPVMYTYDEYIKGYLDQASGSAVIDLTENDQVWLQLPNAGSNGLYSPEYVHSSFSGFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGPRGNAGEPGLPGPPGPPGQVALPEDFVKAGQRPFVSANQGVTGMPVSAFTVILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VFSMYSYE--MKGKSDTSSNHAVLKLAKGDEVWLRMGN---GALHGDHQRFSTFAGFLL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAVGAPIPEDEILYNRQQHYDPRSGIFTCKIPGIYYFSYHV--HVKGTHVWVGLYKNGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPGLPGPPGPPGQAVMPDGFIKAGQRPRLSGMPLVSANHGVTGMPVSAFTVILSKAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.1%;
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                                                                                                                                                                                                                                       analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 275; DB 2; Pred. No. 6.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                       and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bovine
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                                                                                                                                                                                                                                                                                                                                            20-Aug-1999
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A;Molecule type: mRNA
A;Residues: 547-656 <RE2>
A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796
A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014)
A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014)
A;Note: sequence extracted from NCBI backbone (NCBIN:59012, NCBIP:69014)
A;Note: sequence extracted from NCBIP:69014
A;Note: sequence extracted from NCBIP:69014
A;Note: sequence extracted from NCBIP:69014
A;Note: sequence extracted fro
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A; Residues: 'TIPFYGMYCMYCLL',52-680 <APT>
A; Cross-references: EMBL:X65120; NID:g23129
A; Note: the initial difference is probably due
R; Apte, S.; Mattei, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
                                                                                                                                                                                                                                                                       A;Title: In situ hybridization studies on the expression of type X collagen A;Reference number: A43901; MUID:92077285; PMID:1743401 A;Accession: A43901
                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in R;Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, Upper, Biol. 148, 562-572, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Cloning of human alpha-1(X) collagen DNA and localization A;Reference number: S15826; MUID:91243838; PMID:2037056 A;Accession: S15826
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C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999
C;Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856
C;Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856
R;Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.; BeFEBS Lett. 311, 305-310, 1992
R;BES Lett. 311, 305-310, 1992
A;Title: Genomic organization and full-length cDNA sequence of human collagen
A;Reference number: S26396; MUID:93012005; PMID:1397333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 561-647,'G',649-666 <AP2>
A;Cross-references: EMBL:X58879; NID:g30013; PIDN:CAA41686.1; PID:g30014
R;Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solom Biochem. J. 280, 617-623, 1991
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A; Residues: 1-680 < REI>
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A; Residues: 1-26,'T',28-680 <THO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 GEKGYPGIP-----PELQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 YNPSTGKFTCEVPGLYYFVY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 GCYGIPGMPGMPGAPGKDGHDGLQGPKGEPGIPAVPGTQGPKGQKGEPGMPGHRGKNGPR
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Pred. No. 2.8e-15;
of
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C; Superfamily: complement Clq carboxyl-terminal homology

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C;Keywords: coiled coil; extracellular matrix;
F;1-18/Domain: signal sequence #status predicte
A; Experimental source: adult C; Genetics: A; Note: DKFZp586B0621.1.
                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <OTT>
                                                                                                                                                                         submitted to the Protein S. A; Reference number: Z18184 A; Accession: T14782
                                                                                                                                                                                                                                                                            hypothetical protein DKFZp586B0621.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
C;Accession: T14782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Complex: type X collagen
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia C; Complex: type X collagen may be a homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:128635; OMIM:120110 A: Map position: 6q21-6q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:S68531; NID:g545180; PIDN:AAC60 A;Note: mutant sequence from patient with metaphyseal A;Note: a second mutant sequence with 614-Pro is also C;Comment: Prolines and lysines at the third position ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: translated from GB/EMBL/DUBA
A:Molecule type: mRNA
A;Residues: 520-597,'D',599-680 <WAL>
                                                                                                                                                                                                                                                      R;Ottenwaelder, B.; Obermaier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be important for skeletogenesis
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                                                                          A;Cross-references: EMBL:AL110261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: I51870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;520-680/Domain: amino-terminal nonhelical #status predicted <NCl>;53-679/Domain: complement Clq carboxyl-terminal homology <ClQ>;617/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GN---GALHGDHQRFSTFAGFLL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPGPVGPA--GAKGMPGHNGEAGPRGAPGIPGTRGPIGPPGIPGFPGSKGDPGSPGPPG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYFSYHV--HVKGTHVWVGLYKNGTPVMYTYDEYTKGYLDQASGSAIIDLTENDQVWLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGIATKGLNGPTGPPGPPGPRGHSGEPGLPGPPGPPGPPGQAVMPEGFIKAGQRPSLSG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KGDLGPRGERGQHGPKGEKGYPGIP-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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28.5%;
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                                                                                                                                                                                                                                                      В.
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Pred. No. 1.7e-14;
                                                                                                                                                                                                                            Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        677
                                                                                                                                                                                                                                                      Mewes, H.W.;
                                               clone DKFZp586B0621
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                                                                                                                                                                                                                               August
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                                                                                                                                                                                                                                                      Gassenhuber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 680;
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A;Molecule type: mRNA
A;Residues: 1-744 <YAM>
A;Residues: 1-744 <YAM>
A;Residues: GB:J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896
A;Cross-references: GB:J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896
C;Superfamily: collagen alpha 1(VIII) chain; complement C1g carboxyl-terminal
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F;21-117/Region: amino-terminal nonhelical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 264, 16022-16024, 1709
A;Title: The cloning and sequencing of alphal(VIII) collagen omains similar to those of type X collagen.
A:Deference number: A34246; MUID:89380199; PMID:2476437
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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F;572-744/Region:
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                                                                           AYHV--HCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSE
                                                                                                                                                                                                                                                                                                                 GIPGD--QGLQGPPGIPGITGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGKPGVAGLHGP 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVWVQVGVGDYIGIYASIKTDSTFSGFLVY
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                                                                                                                TFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN-
                                                                                                                                                                                                                                                                          KGDKGDLGPRGERGQHGPKGEKGYPGIP------PELQI------
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QAAGLYAGQYVHSSFSGYLLY
                                  --GALHGDHQRFSTFAGFLLF
                                                                                                                                                       KKGKNGGPAYEMPAFTAELTAPFPPVGAPIKFDRLLYNGRQNYNPQTGIFTCEVPGVYYF
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carboxyl-terminal nonhelical
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                                                                                                                                                                                -AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFF 165
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Pred. No. 1.5e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 258.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homolog
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F;21-117/Region: amino-terminal nonhelical
F;118-571/Region: interrupted helical
F;572-744/Region: carboxyl-terminal nonhelical
F;617-743/Domain: complement Cla assessment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Ninomiya, Y. Bur. J. Biochem. 197, 615-622, 1991
A;Title: The complete primary structure of the human alpha-1(VIII) chain and A;Reference number: S15435; MUID:91231001; PMID:2029894
A;Accession: S15435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 13-Jan-1995 #sequence_revision
C;Accession: S15435
                                               A;Reference number: A90304; MUID:80020137; A;Accession: A03207
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A;Map position: 3q11.1-3q13.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЪ
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A; Molecule type: protein
A; Residues: 29-56,'p',58-65,'K',67-71,'p',73-83,'K',85-86,'D',88-89,'N',91-122
C; Comment: The first component of complement is a calcium-dependent complex of
                                                                                                         Biochem. J. 179, 367-371, 1979 A; Title: Complete amino acid s
                                                                                                                                                    R; Reid, K.B.M
                                                                                                                                                                         A; Molecule type: I
A; Residues: 1-245
                                                                                                                                                                                                                                        A; Reference number: A; Accession: S14351
                                                                                                                                                                                                                                                            A; Title: Characterization and organization A; Reference number: S14350; MUID:91174759;
                                                                                                                                                                                                                                                                                                       Biochem. J. 274, 481-490, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                 N; Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                   complement subcomponent Clq chain C precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:COL8A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-744 < MUR>
                                                                                                                                                                                                                                                                                                                                                                  ;Species: Homo sapiens (man);Date: 22-May-1981 #sequence_revision 31-May-1986 #text_change
                                                                                                                                                                                                                                                                                                                             ;Sellar, G.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                             Accession: S14351; A03207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:x57527; NID:g30081; PIDN:CAA40748.1; PID:g30082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
                                                                                                                                                                                                                   Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               722 QAAGLYAGQYVHSSFSGYLLY 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     664 AYHV--HCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          604 KKGKNGGPAYEMPAFTAELTAPFPPVGGPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNG-----NNGATGHEGAKGE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIPGD--QGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFPGIGKPGVAGLHGP 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GALHGDHQRFSTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78;
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                                                                                                                                                                                                                                                                                                                           ; Blake,
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                                                                                                                                                                             SEL>
                                                                                                                                                                                                                                                                                                                                                                                                                 complement subcomponent
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                                                                                                                                                                                                                                                                                                                           D.J.; Reid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.8%;
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                                                                                                                                                                                                                                                                                                                             K.B.M
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                                                                                       the three collagen-like; PMID:486087
                                                                                                                                                                                                                                                                                                                                                                                                               C1q
                                                                                                                                                                                                                                                              of the genes
PMID:1706597
                                                                                                                                                                                                                                                                                                                                                                                                                 gamma chain
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                                                                                                            regions
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    <REI>
                                                                                                                                                                                                                                                                                       C-chain:
                                                                                                              'n
      three
                                                                                                              sut
                                                                                                                                                                                                                                                            A;Residues: 28-253 <RE1>
A;Cross-references: EMBL:X03084
A;Note: the authors translated
R;Reid, K.B.M.
                    A;Title: Amino acid sequence of the N-terminal 108 amino A;Reference number: A90301; MUID:79041552; PMID:708376 A;Accession: A90301
                                                                                                                                                                                                                                                                                                                                                                        A; Note: the authors translated A; Accession: A23422
                                                                                     A; MoLecule type: protein
A; Residues: 'E', 29-84, 'D', 86-99, 'P', 101-135
R; Reid, K.B.M.; Thompson, E.O.P.
Biochem. J. 173, 863-868, 1978
                                                                                                                                                                                                                      A; Title:
                                                                                                                                                                                                                                          Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 'HS', 1-32 <REI>
                                                                                                                                                                         A; Accession: B90304
                                                                                                                                                                                                 A; Reference number:
                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
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Complete amino J. 179, 367-371,

7-371, 1979 mino acid sequences of A90304; MUID:80020137;

the three collagen-like; PMID:486087

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complement subcomponent C1q chain B precursor [validated] - human N;Alternate names: complement subcomponent C1q beta chain C;Species: Homo sapiens (man) C;Date: 22-May-1991 #sequence_revision 31-May-1996 #text_change 08-Dec-2000 C;Accession: B23422; A23422; B90304; A90301; B90315; A03206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;57,72,75/Modified site: 5-nyaroxyiys
F;75/Binding site: carbohydrate (Lys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;32/Disulfide bonds: interchain #status experimental F;36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline F;57,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: complement subcomponent C1q chain A; con C;Keywords: complement pathway; glycoprotein; homodime: F;1-28/Domain: signal sequence #status predicted <SIG>
Biochem. J. 231, 729-735, 1985
A;Title: Molecular cloning and characterization of the complementary DNA and A;Reference number: A23422; MUID:86076906; PMID:3000358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 1p36.3-1p34.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                            CIHUQB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;31-114/Domain: collagenous, triple helix <COL>
F;31-244/Domain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:29-245/Product: complement subcomponent Clq chain B #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB:C1QG
                                                                                                           R; Reid; K.B.M.
                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lvation of Clr (enzyme), Cls (proenzyme), and the other eight components of complemen C;Comment: The Clq subcomponent is composed of nine subunits, six of which are disulf dimers of the C chain. Equimolar amounts of the A, B, and C chains are found after r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 GNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTS 204
                                                                                                                                                                                                                                                                                                                                                                                       204
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SNHAVLKLAKGDEVWLRMGN-----GALHGDHQRFSTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGDYDTSTGKFTCKVPGLYYFVYHA---SHTANLCVLLYRSGVKVVTFCGHTSK-TNQVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPMGPPGMPGVPGPMGIPGEPGEEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVLTNP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDLGPRGERGQHGPKGEKGYPG----IPPELQIAFMASLATHF-SNONSGIIFSSVETNI 144
                                                                                                                                                                                                                                                                                                                                                                                    SGGVLLRLQVGEEVWLAVNDYYDMVGIQGSD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GAPGKDGYDGLPGPKGEPGIPAIPGIRGPKGQKGEPGLPGHPGKN 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.7%;
33.5%;
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Pred. No. 1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          -SVFSGFLLF
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                                                                                                                                                                                                                                                                                                                                                                                          243
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collagen alpha 1(VIII) chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Rosidues: 136-253 <RE4>
A;Rosidues: 136-253 <RE4>
A;Note: 176-Glx may also be present
C;Comment: The first component of complement is a calcium-dependent complex of the three ivation of Clr (enzyme), Cls (proenzyme), and the other eight components of complement.
C;Comment: The Clq subcomponent is composed of nine subunits, six of which are disulfide (see PIR:ClHUQC) chain. Equimolar amounts of the A, B, and C chains are found after redu
Š
                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-744 <NIN>
                                                                                                                                                                                                                                                           A; Reference number: S22243
A; Accession: S23298
                                                                                                                                                                                                                                                                                                       in Extracellular Matrix Genes, A; Title: The molecular biology
                                                                                                                                                                                                                                                                                                                                                         R;Ninomiya, Y.; Castagnola, P.; maguchi, N.; Olsen, B.R.
                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F; 28-253/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1p36.3-1p34.1
C; Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal hon
C; Keywords: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyproline
C; Keywords: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyproline
F;1-27/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. J. 203, 559-569, 1982
A;Title: Completion of the amino acid sequences of the A and A;Reference number: A90315; MUID:82283890; PMID:6981411
A;Accession: B90315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:119043; OMIM:120570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB:C1QB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                     Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxy1-terminal homology 617-743/Domain: complement Clq carboxy1-terminal homology <ClQ>
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   K.B.M.; Gagnon, J.; Frampto
. J. 203, 559-569, 1982
                                                                       Tocal
GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEMKGKSDTSSNHAVLKLAKGDEVWLR-MGNGALHGDHQRFSTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNYEPRSGKFTCKVPGLYYFTYHASSRGNLCVNLMRGRERAQKVVTFCDYAYNTF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFFDVMTGRFGAPVSGVYFFTFS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QHGPKGEKGYPGIP------PELQIAFMASLATHFS-NONSGIIFSSVETNIG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGPPAIPGIPGIPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNPGKVG
                                                                  Similarity
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31.7%;
                                                                  18.4%;
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                                                                                                                                                                                                                                                                                                       Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre of collagens with short triple-helical domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                               Gerecke,
                                            Score 251.5;
Pred. No. 6.2e
24; Mismatches
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Pred. No. 2.1e-13;
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                                                                  6.2e-13;
                                                                                                                                                                                                                                                                                                                                                                            Gordon, M.K.;
                                                                                        DB 1;
                                              104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 253;
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                                              Indels
                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                               Jacenko,
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                                              55;
  KGE 85
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                                              Gaps
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collagen alpha 1(VIII) chain
                                              RESULT 14
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C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carbo F;1-11/Domain: amino-terminal nonhelical (fragment) #status prediff;2-46B/Region: interrupted helical F;12-46B/Region: interrupted helical F;469-635/Domain: carboxyl-terminal nonhelical #status predicted F;508-634/Domain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A57131; MUID:91210292; PMID:2019595 A;Accession: A57131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Muragaki, Y.; Jacenko, O.; Apte, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R. J. Biol. Chem. 266, 7721-7727, 1991
A;Title: The alpha2(VIII) collagen gene. A novel member of the short chain col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: A57131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collagen alpha 2(VIII) chain - human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: COL8A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-635 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
629
                                                   239
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                                                                                                                                                                                                                                                                                                                                                                                                                395 GPSGIPGLQGPAGPIGPQGLPGLKGEPGLPGPPG-EGRAGEPGTAGPRGPPGVPGSPGIT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 GDYSFRGYQGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPK 104
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                                                GFLLFET 245
                                                                                                    YKNNVPATYTYDEYKKGYLDQASGGAVLQLRPNDQVWVQIPSDQANG-LYSTEYIHSSFS
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GFLLCPT
                                                                                                                                                 NGNTVFSMYSYE--MKGKSDTSSNHAVLKLAKGDEVWLRM----GNGALHGDHQRESTFA 238
                                                                                                                                                                                                        TSPLPASGMPVKFDRTLYNGHSGYNPATGTFTCPVGGVYYFAY----HVHVKGTNVWVAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Similarity
| 76; | Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 249; DB 2; Pred. No. 8.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                               -----PELQI-----AFMASL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
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mouse

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C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S23779
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A; Accession: S19018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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R;Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Ninomiya, Y.

Eur. J. Biochem. 207; 895-902, 1992

Eur. J. Biochem. 207; 895-902, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement subcomponent C1q chain A precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
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A; Residues: 1-743 <MUR>
                                            Q
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C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal homeofic complement complement clauses and component clauses are complement clauses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-245 < PET>
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Best Local Similarity 29.59
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664 YHV--HCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQASGSAVLLLRPGDQVFLQNPFEQ 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 FSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLR----M
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150
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                                               154 RFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG--NTVFSMYSYEMKGKSDTSSNHAVLK 211
                                                                                                                                                                                                                                                                                                                       Local Similarity hes 71; Conserv
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                                                                                                                                                                                                               31
                                                                                                                                                                                                                                        51 GYQGPPGPPGIPGNHGNNGNNGATG-HEGAKGEKGDKGD------LGP 94
RFICAVPGFYYFNFQVISKWDL-CLFIKSSSGGQPRDSLSFSNTNNKGLFQVLAGGTVLQ 208
                                                                                                    LGDSGPQGLKGVKGNPGNIRDQPRPAFSAIRQNPMTLGNV-VIFDKVLTNQESPYQNHTG
                                                                                                                                                       RGERGOHGPKGEKGYPG-IPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTG 153
                                                                                                                                                                                                            GKDGAPGNPGRPGRKGERGEPGAAGIRTGIRGFKGDPGESGPPGKPGNVGLPGPSGP 90
                                                                                                                                                                                                                                                                                                                       Conservative
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Qy 212 LAKGDEVWLRM--GNGALHGDHQRFSTFAGFLLF 243
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| Db 209 LRRGDEVWLEKDPAKGRIYQGTEADSIFSGFLIF 242
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Search completed: January 15, 2003, 19:40:47 Job time : 50 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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bos taurus
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rattus norv
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homo sapien
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sapien
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DR DR DR FT

SIGNAL CHAIN

22 246

POTENTIAL.

COMPLEMENT-CLQ TUMOR NECROSIS FACTORRELATED PROTEIN 3.

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Best Local Similarity
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                       EMBL; AF329839; AAK17963.1; -.
EMBL; BC022187; AAK12187.1; -.
Genew; HGNC:14342; C1QTWE7.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q. 1.
Pfam; PF01391; Collagen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _HUMAN
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CONFLICT
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                  Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases --- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN. --- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complement-clq tumor necrosis factor-related C1QTNF7 OR CTRP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQT7
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                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                 iddington C.S., Sheppard P.O., Bishop P., Lasser G.W.; Homo sapiens complement-clq tumor necrosis factor-related ubmitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLFETK 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246;
SM00110; C1Q; 1.
                                                                                                                                                                                                         the Swiss Institute of Bioinformatics
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114
214
246
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246
214
26994
             COMPLEMNTC1Q
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RESULT 3
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Best Local
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DOMAIN
SEQUENCE
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Collagen;
SIGNAL
         EMBL; AF329836; AAK17960.1;
EMBL; BC011699; AAH11699.1;
Genew; HGNC:14325; ClQTNF2.
Interpro; IPR001073; Clq.
                                                                                                                                                                                       Submitted (JUL-2001) to the EMBL/GenBank/DDBJ-!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN-!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                           Piddington C.S., Bishop P.;
"Homo saplens complement-clq tumor necrosis factor-related "Homo saplens complement clq tumor necrosis factor-related committed (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                              Complement-clq tumor necrosis factor-related protein C1QTNF2 OR CTRP2.
                                                                              or send an
                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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                                                                                                                                                  between
                                                                                                                                                                                                                                               TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGKFICAFPGIYYFSYDITLANKH-----LAIGLVHNG-----QYRIKTFDANTGNH
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                                                                                                                                            the Swiss Institute of Bioinformatics
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                                                                              email to license@isb-sib.ch).
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289
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30683
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289
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Pred. No. 1.3e-1
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COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285
                                                                                                                   There are no restrictions on ong as its content is in no
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                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96;
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                                                                                                                                                 EMBL outstation
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IPR000087;

Clq. Collagen

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RESULT 4
C1RF_HUMAN
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CIRE_HUMAN 5.....
075973;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence updated)
16-OCT-2002 (Rel. 41, Last annotation updated)
15-TIN-2002 (Rel. 41, Last annotation updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                 Berube N.G., Swanson X.H., Bertram M.J., n.z...
Berube N.G., Swanson X.H., Bereira-Smith O.M.;
Baskin D.S., Smith J.R., Pereira-Smith O.M.;
"Cloning and characterization of CRF, a novel Clq-related factor,
"Cloning and characterization of the company of the brain involved in motor function.";
expressed in areas of the brain involved in motor function.";
                                                                                                         Nickerson
Submitted
       Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM.
-!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
-!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                        Strausberg R.;
                                                                     TISSUE=Placenta;
                                                                                  SEQUENCE FROM
                                                                                                                                  Rieder M.J.,
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99097006; PubMed=9878755;
                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01113; C10; 1.
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SMART; SM00110; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVHNGQ--YRIRTFDANTGNHDVASGSTILALKQGDEVWLQIFYSEQNGLFYDPYWTDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKSYPRERLPIKFDKILMNEGGHYNASSGKFVCGVPGIYYFTYDITLANKH-----LAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATHESNQNSGIIFSSVETNIGNEFDVMTGREGAPVSGVYFFTTSMM---KHEDVEEVYVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GER-----PELQIAFMASL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLPGPQGPPGPPGAPGPSGMMGRMGFPGKDGQDGHDGDRGDSGEEGPPGRTGNRGKPGPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTGFLIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMHNGNTVFSMYSYEMK-GKSDTSSNHAVLKLAKGDEVWLRM----GNGALHGDHQRFST
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PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                          (AUG-2001)
                                                                                                                     D.A.;
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143
285 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       276
                                                                                                                               Carrington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
285
29952 MW;
                                                                                                                                                                                                                                                                              Chordata;
Primates;
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285
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                                                                                                          the
                                                                                                                                 D.P.,
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                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C1Q.
; 7E31FF9868D4EDFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 304; DB 1;
Pred. No. 1.1e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELATED PROTEIN 2. COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
                                                                                                                               Chung M.-W.,
                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                           258
                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                           AΑ
                                                                                                                                                                                                                                                                                Hominidae;
                                                                                                                               Lee K.L., Poel C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                         Euteleostomi;
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RESULT 5
CIRF_MOUSE
ID CORF_M
AC 088992
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT 16-OCT
OC CORF (
OS Mus mus
OC Eukary
OC Mammal.Tr
OX NCBL_Tr
RN [1]
RN [1]
RN [2]
RN BERUBER
RA BERUBER
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InterPro; IPR001073; C1q,
InterPro; IPR0001087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC10.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C1RF_MOUSE
088992;
Berube N.G., Swanson X.H., Bertram M.J., Kittle J.D., Didenko V., Baskin D.S., Smith J.R., Pereira-Smith O.M.;

"Cloning and characterization of CRF, a novel Clq-related factor, expressed in areas of the brain involved in motor function.";

Brain Res. Mol. Brain Res. 63:233-240(1999)

-!- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM. MORE ABUNDANT IN AREAS OF THE NERVOUS SYSTEM INVOLVED IN MOTOR FUNCTION, SUCH AS THE PURKINJE CELLS OF THE CEREBELLUM, THE ACCESSORY OLIVARY NUCLEUS, THE PONS AND THE RED NUCLEUS.

-!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
Clq-related factor pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clorf or CRF.
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                                                                                                                                                                                                                                                                                         MEDLINE=99097006; PubMed=9878755;
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPOTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGD 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGNNYDAASGKFTCNIPGTYFFTYHVLMRGGDGTSMWADLCKNGQVRASAIAQDADQNYD
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17
67
123
258 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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258
115
258
                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52C51CDF59CAE2BF CRC64;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       APMI_MOUSE STANDARD; rni, 260994; 062400; Q9D568; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Adiponectin precursor (30 kDa adipocyte complement-related adiponectin precursor specific protein AdipoQ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                              TISSUE-Adipocyte;
MEDLINE-96070757;
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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  MEDLINE=96209999;
Hu E., Liang P., :
                                            SEQUENCE FROM N.A. TISSUE-Fibroblast;
                                                                                                                                        adipocytes.";
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                     (ACRP30) (Adipocyte specific protein APM1 OR ACRP30 OR ADIPOQ.
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InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                                                                                                                                                        Scherer P.E., Williams A novel serum protein
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European Bioinformatics Institute. There are no
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; PF01391; Collagen; 1.
rr; PR00007; COMPLEMNTC1Q.
rr; SM00110; C1Q; 1.
iTE; PS01113; C1Q; 1.
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Spiegelman B.M.;
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ilar to Clq, p
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C1Q-RELATED FACTOR.
COLLAGEN-LIKE.
C1Q.
KM; F776E2D206EBF763 CRC64;
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Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yar
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T.,
                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ED
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Berg A.H., Combs T.P., Du X., Brownlee
"The adipocyte-secreted protein Acrp30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The fat-derived hormone adiponectin reverses i associated with both lipoatrophy and obesity.";
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Froguel P., Kadowaki T.;
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Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka
Akanuma Y., Gavrilova O., Vinson C., Reitman M.I
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J. Biol. Chem. 271:10697-10703(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Chromosomal localization,
                                                                                                                                                                                                                              EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. CONTROL OF FAT METABOLISM AND INSULIN SENSITI SUBUNIT: HOMOOLIGOMER. SECRETED IN PLASMA. TISSUE SPECIFICITY: SYNTHESIZED EXCLUSIVELY B
                                                                                                                                           ACTIVATED BY INSULIN SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                   FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITS ENDOTHELIAL NE-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS THE-ALPHA-INDUCED
                                                                                                                                                                                               INDUCTION: DURING
                                                                                                                                                                                                              SECRETED INTO SERUM
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                                                                                                                                           1 COLLAGENOUS DOMAIN.
1 C1Q DOMAIN.
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Fukuda S.,
manaka I.,
Saito R.,
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                                                                                                                                                                                                    RESULT
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Best Local S
Matches 81
                                                                                                                                              11_HUMAN
APM1_HUMAN
Q15848;
                                                                                    01-NOV-1997
01-NOV-1997
15-JUN-2002
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CONFLICT
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MOD_RES
VARIANT
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SEQUENCE
             APM1 OR ACRP30 OR GBP28.
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Pfam; PF01391; Collagen; 1.
                                                                       Adiponectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001073; Clq. InterPro; IPR000087; Collagen.
                                                 (ACRP30) (Adipose most abundant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hormone;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:106675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                116
                                                                                                                                                                                                                                                                                          227 LHGDHQRFSTFAGFLLF 243
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                                                                                                                                                                                                                                                                                                                                                    HPGHNGTPGRDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGER----GQHGPKGEKGYPGIPPE----
                                                                                                                                                                                                                                                         LYADNVNDSTFTGFLLY 243
                                                                                                                                                                                                                                                                                                                               VY--MKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDHNG
                                                                                                                                                                                                                                                                                                                                                                                                      EAAYMYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHIT
sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIYWQLLALFFLPFCLCQDEYMESPQTGG--LPPDCSKCCHGDYSFRGYQGPPGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U37222; AAA80543.1; -. U49915; AAB06706.1; -. AF304466; AAK13417.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK003138; BAB22597.1; -
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SM00110; C1Q; 1.
E; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collagen;
                              (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
precursor (30 kDa adipocyte complement-related and precursor (30 kDa adipocyte complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148
243
247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
(Human)
                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROXYLATION
M -> V.
P -> S (IN REF
A -> S (IN REF
A -> G (IN REF
G -> N (IN REF
Y -> F (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 294; DB 1;
Pred. No. 6.5e-18;
0; Mismatches 102
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HYDROXYLATION
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HYDROXYLATION
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COLLAGEN-LIKE.
                                                                                                                                                                 PRT;
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                                                 (Gelatin-
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OOC COCKETT TO A SECRET TO A S
VARIANTS ARG-84; MET-117; THR-164; SER-221 MEDLINE=21671103; PubMed=11812766; Hara K., Boutin P., Mori Y., Tobe K., Dina Otabe S., Okada T., Eto K., Kadowaki H., Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H., Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y., Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.; "Adiponectin, an adipocyte-derived plasma protein, inhibits endothelial NF-kappaB signaling through a cAMP-dependent pathway."; Circulation 102:1296-1301(2000).
                                                                                                                                                             adiponectin.";
                                                                                                                                                                                                                  Takahashi M., Arita Y., Yamagata K., Matsukawa Y., Okutomi K.
Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara S., Nal
Yamashita S., Funahashi T., Matsuzawa Y.;
                                                                                                                                                                                                                                                                                                 VARIANT ADIPONECTIN DEFICIENCY CYS-112. MEDLINE-20378830; PubMed-10918532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Froguel P., Kadowaki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamauchi T., Kamon J., Waki H., Terauchi Y., Kubota
Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N.,
Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., I
Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
MEDLINE=20440368; PubMed=10982546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Adiponectin, a new member of the family of soluble defense collagens, negatively regulates the growth of myelomonocytic progenitors and the functions of macrophages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsuzawa Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE 20417747; PubMed-10961870;
MEDLINE 20417747; PubMed-10961870;
Yokota T., Oritani K., Takahashi I., Ishikawa J.
Ouchi N., Kihara S., Funahashi T., Tenner A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 1q21.3-q23, a susceptibility locus identified combined hyperlipidemia (FCH)."; biochem. Biophys. Res. Commun. 260:416-425(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The human apM-1, an adipocyte-specific gene linked TNF's and to genes expressed in activated T cells, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=99333693; PubMed=10403784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito K., Tobe T., Minoshima S., Asakawa S., S
Nakano Y., Shimizu N., Tomita M.;
"Organization of the gene for gelatin-binding
Gene 229:67-73(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96224171; Pu
Maeda K., Okubo K.,
                                                                                                                                                                                            "Genomic structure and mutations
                                                                                                                                                                                                                                                                                                                                                                                                              associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21372498; PubMed=11479627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-99196984; PubMed-10095105;
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factor, apm1 (AdiPose Most abundant Gene transcript 1).";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                fat-derived hormone adiponectin reverses insulin resistance clated with both lipoatrophy and obesity.";
                                                                                                                                         Obes. Relat.
                                                                                                                                                                                                                                                                                                                                                                               7:941-946(2001).
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                                                                                                                                         Metab.
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Y., Tobe K., Nagai R., Kimura
                                                                                                                                         Disord.
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suboyama-Kasaoka N., Ezaki O.,
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                                                                                                                                      24:861-868(2000)
                              Dina C.,
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  Hagura
                                                                                    AND PRO-241.
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Yasuda K., Ya
a R., Akanuma
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                              Yamauchi
                                                                                                                                                                                                                                              Nakamura T.,
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-I- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS INFORMATION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.

-I- SUBCUNIT: HOMOOLIGOMER (POTENTIAL).
-I- SUBCELIULAR LOCATION: SECRETED IN PLASMA.
-I- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE ADIPOSE TISSUE.
-I- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE ADIPOSE TISSUE.
-I- DISEASE: Defects in APMI are the cause of adiponectin deficiency, resulting in very low concentration of plasma adiponectin.

Decreased adiponectin plasma levels are associated with obesity insulin resistance, and diabetes type 2.
-I- PHARMACEUTICAL: Adiponectin might be used in the treatment of diabetes type 2 and insulin resistance.
-I- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
-I- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
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DOMAIN
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MOD_RES
MOD_RES
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EMBL; AB012164; BAA86716.1; JOINED
EMBL; AJ131460; CAB52413.1; -.
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                                                        VARIANT
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SMART; SM00110; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
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         CARBOHYD
                                  DOMAIN
                                                                      SIGNAL
                                                                                Collagen;
                                                                                                                                Pfam; PF00386; C1q; 1. Pfam; PF01391; Collagen;
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InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2002) to the EMBL/GenBank/DDBJ-1-SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN-1-SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                             "Homo sapiens complement-clq tumor necrosis factor-related protein."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Piddington C.S., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C1QTNF6 OR CTRP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-clq tumor necrosis factor related
                                                         CHAIN
                                                                                              PROSITE; PS01113; C1Q;
                                                                                                             SMART;
                                                                                                                      PRINTS;
                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                AF329842; AAK17966.1; -. BC020551; AAH20551.1; -. BC020551; AAH20551.1; -. BC02:14343; C10TNF6;
                                                                                                          SM00110; C1Q;
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                                                                                                                      PR00007;
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Primates;
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Pred. No. 7.1e
35; Mismatches
C1Q.
N-LINKED (GLCNAC.
                               RELATED PROTEIN COLLAGEN-LIKE.
                                                         COMPLEMENT-C1Q TUMOR NECROSIS FACTOR
                                                                     POTENTIAL.
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SEQUENCE
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Collagen;
                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See )
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- TISSUE SPECIFICITY: EXPRESSED IN GLIAL CELLS.
-1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
-1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koide T., Aso A., Yorihuzi T., Nagata K.;
"Conformational requirements of collagenous peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=20428709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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16-OCT-2001
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    SEQUENCE
                            DOMAIN
                                                                          CHAIN
                                                                                                  SIGNAL
                                                                                                                                                                   SMART;
                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 RVWVRLFKRQRENAIYSNDFDTYITFSGHLI
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Biol. Chem. 275:27957-27963(2000).
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  POTENTIAL.
GILACOLIN.
COLLAGEN-LIKE.
C10.
; 529FBAF4B2191BC1 CRC64;
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27A82CA863F23D47 CRC64;
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RESULT 10
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Best Local
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01-NOV-1991 (Rel. 20, Last sequence
15-JUL-1999 (Rel. 38, Last annotatio
Collagen alpha 1(X) chain precursor
COLLOAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA1A_CHICK
P08125;
                                                                                                                                                           WEDLINE-89380199; PubMed-2476437;
Yamaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;
Yamaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;
The cloning and sequencing of alpha 1(VIII) collagen cDNAs
demonstrate that type VIII collagen is a short chain collagen and
contains triple-helical and carboxyl-terminal non-triple-helical
domains similar to those of type x collagen.";
J. Biol. Chem. 264:16022-16029(1989)
-i- FUNCTION: TYPE: X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC
CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    open
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between the Swiss Institute of Bioinformatics and the EMBL outstation - between the Swiss Institute of Bioinformatics and the EMBL outstation on its
                                                                                                                                                                                                                                                                                                                                                 Luvalle P., Ninomiya Y., Rosenblum N.D., Olsen B.R.;
"The type X collagen gene. Intron sequences split the 5'-untranslated region and separate the coding regions for the non-collagenous aminoterminal and triple-helical domains";
J. Biol. Chem. 263:18378-18385(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ninomiya Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89054019; PubMed=2461368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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                                                            PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS. SIMILARITY: CONTAINS 1 C10 DOMAIN.
                                                                                                                                SUBUNIT: HOMOTRIMER
                                                                                                                                               MINERALIZATION ZONES OF HYALINE CARTILAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmentally regulated type X reading frame without introns."; iol. Chem. 261:5041-5050(1986).
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01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last seq

01-NOV-1995 (Rel. 32, Last ann

~~11agen alpha 1(X) chain prec
MEDLING N., Eerola I., Rosatı n., ....
Elima K., Eerola I., Rosatı n., ....
de Crombrugghe B., Vuorio E.;
"The mouse collagen X gene: complete nucleotide
"The mouse collagen X gene: complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by
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Mammalia; Eutheria;
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MEDLINE-93143676;
                                                                                                                                          SEQUENCE FROM N.A.
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Pfam; PF01391; Collagen; 8.
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InterPro; IPR000087; Collagen
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EMBL; J04194; AAA48634.1;
PIR; A31896; A31896.
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Sciurognathi; Muridae;
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EMBL; X67348; CAA47763.1; -.
EMBL; X65121; CAA46237.1; -.
EMBL; X63013; CAA44741.1; -.
EMBL; Z63010; CAA79736.1; -.
PIR; S28807; S28807.
PIR; S31216; S31216.
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Biophim. Biophys. Acta 1130:78-80(1992).
PICTION: TYPE X COLLAGEN IS A PRODUCT OF CHONDROTOCYTES AND HAS BEEN LOCALIZED TO FOR MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elima K., Metsaeranta M., Kallio J., Po
Garofalo S., de Crombrugghe B., Vuorio
"Specific hybridization probes for mous
                                                                                                                                         PRINTS; PRO0007; COMPLEMNTC1Q.
PRODOMS; PD000007; Collagen; 2.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Intron-exon structure, alternative use of promoter and the mouse collagen X gene, Coll0a-1.";
Eur. J. Blochem. 213:99-111(1993).
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                                                                                                                   Cartilage; Collagen;
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or send an email to license@isb-sib.ch).
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InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
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MEDLINE=9111313; PubMed=1703407;
Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.;
Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.;
         EMBL; X53556; CAA37624.1; PIR; S13301; S13301. InterPro; IPR001073; C1q. InterPro; IPR000087; Colla
                                                                                                                                                                                                                                                        Biochém. J. 273:141-148(1991).

- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
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01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                              collagen genes."
                                                                                                                                                                                                                                                                                                                           "Isolation of cDNAs encoding the complete sequence of bovine type collagen. Evidence for the condensed nature of mammalian type {\tt X}
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Bovidae; Bovinae; Bo
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                                                                           non-profit institutions as long d and this statement is not removed s requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
           Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor
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Pred. No. 4.
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A -> C (IN REF. 3).
I -> H (IN REF. 3).
FD -> IY (IN REF. 3).
Q -> T (IN REF. 3).
FE984CA99AF708E2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674
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                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.le-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87;
                                                                                                     Usage
                                                                                                                     its content
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                                                                                                        commercial
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RESULT 1.
C1QC_MOUSE
ID C1QC_MOUSE
Q02105;
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Best Local
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STRAIN=BALB/C: TISSUE=Liver;

MEDLINE=96186528; PubMed=8606057;

MEDLINE=96186528; PubMed=8606057;

Petry F., McClive P.J., Botto M., Morley B.J., Morahan G., L

"The mouse C1q genes are clustered on chromosome 4 and show

"Conservation of gene organization.";

Immunogenetics 43:370-376(1996)

-I- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1:

C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
DOMAIN
                                                                                                                                  precerebellin.";
                                                                                                                                                            coding for the C
                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE-Macrophage;
MEDLINE-93011118; PubMed-1396691;
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                    Complement Clq subcomponent, C chain
                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 01-JUL-1993 (Rel. 16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00007; COMPLEMNTC1Q. ProDom; PD000007; Collagen; 1.
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                        Eur. J. Biochem.
                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00110; C1Q;
                                                                                                                                                                     Isolation,
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                                                                                                                                     NE-93011110; F......
F., Reid K.B.M., Loos M.;
ation, sequence analysis and characterization of cDNA g for the C chain of mouse Clq. Sequence similarity of the C chain of mouse Clq. Sequence similarity of the C chain of clq. collagen type VIII and type X
                                                                                                                                                                                                                                                                                          OR ClQC
                                                                                                                                                                                                                                                                                                                                                                                                                                               GNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRM---GNGALHGDHQRFSTFAGFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QHGPKGEKGYPGIP-----PELQIA----FMASLATHFSNQNSGII------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAYPAIGTPIPFDKILYNKQQHYDPRTGIFTCKIPGIYYFSYHI--HVKGTHAWVGLYKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -FSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHN
                                                                                                                       209:129-134(1992).
                                                                                                                                                                                                                                                                                                         26, Created)
26, Last sequence update)
40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Connective tissue; Repeat; Hydroxylation; Signal; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 275; DB 1
Pred. No. 8e-16;
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BY SIMILARITY
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NONHELICAL REGION (I
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                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD4CA73A03E004CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                     precursor
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SIMILARITY).
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                                                                                                                                                                                                                                                       Murinae;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:88225; C1qc.
InterPro; IPRO01073; C1q.
InterPro; IPRO00087; Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00110; C10; 1
PROSITE; PS01113; C10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      SEQUENCE
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                              199
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199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN INMUNE COMPLEXES.
SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R
AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN. SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT C1R(2)C1S(2) PROENTME COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE C CHAIN.
                                                                                                                                                                                                            GYQGPPGPPGPPGIPGNHGNNGNTGH-----EGAKGEKGDKGDLGPRGERGQHGPK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S29328; S29328
                                                                             GTSGLPGDPGPRGPPGEPGVEGRYKQKHQSVFTVTRQTTQYPEANALVRFNSVVTNPQGH
                                                                                                                                                                              NSKQVSSGGALLRLQRGDEVWLSVNDYNGMV-GIEGSNSVFSGFLLF
                          GKSDTSSNHAVLKLAKGDEVWLRMG--NGALHGDHQRFSTFAGFLLF
                                                                                                                                                GEKGYPGIP-----PELQ-----IAFMASLATHFSNQNSGIIFSSVETNIGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X66295; CAA46993.1;
X92960; CAA63535.1;
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                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathway;
                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                        ME:
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HYDROXYLATION
HYDROXYLATION
                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                       Score 274;
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                                                                                                                                                                                                                                          Mismatches
                                                       --:-YTSHTANLCVHLNLNLARVASECDHMF
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Y SIMILARITY).
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Apte S., Mattei M.-G.,
"Cloning of human alpha
COL10A1 gene to the 921
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE=92109659; PubMed=1764025;
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Mammalia; Eutheria;
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    Boot-Handford R.P.;
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human alpha 1(X) collagen
to the q21-q22 region of
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RT "Novel missense mutation resulting in the substitution of tyrosine by RT cysteine at codon 597 of the type x collagen gene associated with RT Schmid metaphyseal chondrodysplasia.";

RL J. Hum. Genet. 43:259-261(1998).

CC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE COLLAGEN.

CC -!- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC COLLAGEN.

CC -!- SUBUNIT: HOMOTRIMER.

CC -!- SUBUNIT: HOMOTRIMER.

CC -!- DISEASE: DEFECTS IN COLLAGEN OF THE TRIPEPTIDE REPEATING COLLAGEN.

CC -!- DISEASE: DEFECTS IN COLLOGIA ARE THE CAUSE OF SCHMID TYPE METAPHYSEAL CHONDRODYSPLASIA (SMCD), A DOMINANTLY INHERITED COLLAGENOTYPE ARE MILLD SHORT STATURE, COXA VARA AND A WADDLING CALT.

CC PHEMOTYPE ARE MILLD SHORT STATURE, COXA VARA AND A WADDLING CALT.

CC RADIOGRAPHY USUALLY SHOWS SCLEROSIS OF THE RIBS, FLARING OF THE CALT.

CC METAPHYSES, AND A WIDE IRREGULAR GROWTH PLATE, ESPECIALLY OF THE
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MEDLINE=97220591; PubMed=9067753;
Ikegawa S., Nakamura K., Nagano A., Haga N., Nakamura Y.;
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Chan D., Cole W.G., Rogers J.G., Bateman J.F.;
"Type X collagen multimer assembly in vitro is prevented by a G1y618 to Val mutation in the alpha 1(X) NC1 domain resulting in Schmid metaphyseal chondrodysplasia.";
J. Biol. Chem. 270:4558-4562(1995).
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MEDLINE=99069781; Pul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mutation of the type X collagen gene 'COL10A1' causes spondylometaphyseal dysplasia."; Am. J. Hum. Genet. 63:1659-1662(1998).
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MEDLINE=99057503; PubMed=9837818;
Ikegawa S., Nishimura G., Nagai T.,
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Schmid metaphyseal chondrodysplasia locus.";
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Q9BXJO; Q9UFX4;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-clq tumor necrosis factor-related protein 5 precursor.
C1QTNF5 OR CTRP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
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Sheppard P.O., Humes J.M.;
"Homo sapiens complement-olg tumor necrosis factor-related protein.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF329841; AAK17965.1; -. EMBL; AL110261; CAB53702.1; -. Genew; HGNC:14344; C1QTNF5.
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                                                                                                                                                                                                                                                               SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
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!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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                                                 GSPPLDDNKIPSLCPG---HPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRP
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COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
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Search completed: January 15, 2003, 19:38:01 Job time: 40 secs

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Post-processing: Minimum Match 0%
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1: sp_archea:*
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Q8te71 homo sapien
Q9z1k4 rattus norv
Q9h667 homo sapien
Q8te95 homo sapien
Q8te02 mus musculu
Q96d07 homo sapien
Q9d2v4 mus musculu
Q921s8 mus musculu
Q951s6 mus famil
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ALIGNMENTS

RESULT Q9ES30

	1 MLGRORIWHLLPLLFLPFCLCQDEYMESPQAGGLPPDCSKCCHGDYGFRGYQGPPGPPG 60	Db
	1 MLWRQLIYWQLLALF	Qy
0;	Query Match 95.9%; Score 1311; DB 11; Length 246; Best Local Similarity 95.9%; Pred. No. 9.2e-110; Matches 236; Conservative 2; Mismatches 8; Indels 0; Gaps	710
	SEQUENCE 246 AA; 26828 MW; 42A481B3E9F48F7E CRC64;	SQS
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	EMBL; AF	DR
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	skeletal development.";	RT
	encoding a putative secretory protein and its possible involvement in	RT
	"Molecular cloning and characterization of a novel gene, CORS26,	RT
	Maeda T., Abe M., Kurisu K., Jikko A., Furukawa S.;	RA
	MEDLINE=21264842; PubMed=11071891; .	RX
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RA Arakawa T., Hara A., Fukunishi Y., Konno M., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesolè G., Quackebbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesolè G., Quackebbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesolè G., Quackebbush J.,
RA Kuehl P., Lewis S., Watsuo Y., Nikaido I., Pesolè G., Quackebbush J.,
RA Kuehl P., Lewis S., Watsuo Y., Nikaido I., Pesolè G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Mashima J., Mamazarellii J., Mombaerts P.,
RA Gasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Gyrshw-Poris A. Yoshida K., Haserawa Y. Kawaii H. Kohtsuki S.
                                                                            Matches
                                                                                             Query Match
Best Local
                                                                                                                                                     EMBL; AKO07683; BAB25187.1; -. MGD; MGI:1916433; 1810033K05Rik. InterPro; IPRO01073; C1q. InterPro; IPRO00087; Collagen. Pfam; PF00386; C1q; 1. Pfam; PF01391; Collagen; 2. PRINTS; PRO0007; COMPLEMNTC1Q. SMART; SM00110; C1Q; 1. PROSITE; PS01111; C1Q; 1. PROSITE; PS01111; C1Q; 1.
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STRAIN=C57BL/6J; TISSUE=PANCREAS;
MEDLINE=21085660; PubMed=11217851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection.";
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10
                                     6 LIYWQLLALFFLPFCLCQDEYM-----ESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPP 59
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MISWVLLAC-ALP--
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                                                                            Conservative
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-CAADPMLGAFARRDFQKGGPQLVCS-
                                                                                               22.9%;
28.9%;
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17,
17,
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                                                                          Score 313; DB 11;
Pred. No. 3.8e-20;
41; Mismatches 89
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Last annotation update)
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                                                                                                                                                           6D3905AE7C19E6FA CRC64;
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LPGPQGPP 54
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Best Local
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Q95MQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein, Adipo 0.";
J. Biol. Chem. 276:28849-28856(2001).
EMBL; AF269230; AAKS9902.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.; "Identification and Adipocyte Differentiation-dependent Expression the Unique Disialic Acid Residue in an Adipose Tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21369933;
Sato C., Yasukawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TREMBLrel. 19, Created)
01-DEC-2001 (TREMBLrel. 19, Last sequence update)
01-DEC-2002 (TREMBLrel. 21, Last annotation update)
Adipose tissue-specific protein adipo Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191
   191
                                                           203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134
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                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                16
                                                                                                                                                                                                                                                                                                                                                                                               44 HGDYSFRGYQGPPGPPGP-----PGIPGNHGNNGANGATGHEGAKGEKGDKGD----LGPR
                                              TSSNHAVLKLAKGDEVWLRMGNGALH ----GDHQRESTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMM---KHEDVEEVYVYLMHNGNTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPGIPGNHGNNGNNGATGHEGAKGEKGDKGD----
QASGSVLLHLEVGDQVWLQVYEGENHNGVYADNVNDSTFTGFLLY
                                                                                                                                                                              NIGNEFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSD
                                                                                                                                                                                                                                            GETGDVGMTGAEGPRGFPGTPGRKGEPGEAAYVYRSAFSVGLETRVTVPNVPIRFTKIFY
                                                                                                                                                                                                                                                                                                 GER----GQHGPKGEKGYPGIPPE------LQIAFMASLATHFSNQNSGIIFSSVET 142
                                                                                                                                                                                                                                                                                                                                                                HGEDNM----EDPPLPKGACAGWMAGIPGHPGHNGTPGRDGRDGTPGEKGEKGDAGLLGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPRGPKGVSGTPGKHGTPGKKGPKGKKGEPGLPGPCSCGSSRAKSAFSVAVTKSYPRERL 174
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                                                                                                                   NQQNHYDGSTGKFYCNIPGLYYFSYHITVY--MKDVKVSLFKKDKAVLFTYDQYQEKNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMYSYEMK-GKSDTSSNHAVLKLAKGDEVWLRM----GNGALHGDHQRFSTFAGFLLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 299; DB 6;
Pred. No. 5.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C6253BA803B9A668 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 240;
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                                                           243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovoidea;
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RESULT 4 Q95JD7

Q95JD7 Q95JD7;

PRELIMINARY;

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RESULT
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Best Local
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InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF001391; Collagen; 1.
ProDom; PD000007; Collagen; 1.
PROSITE; PS01113; C1Q; UNKNOWN_1.
SEQUENCE 243 AA; 26264 MW; 498
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01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                            SEQUENCE FROM N.A.
MEDLINE=21015405; PubMed=11130976;
Nielsen V.H., Bendixen C., Arnbjer.
Shukri N.M., Thomsen B.;
                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000
01-JUN-2002
  "Abnormal growth plate function in type X collagen.";
Mamm. Genome ll:1087-1092(2000).
EMBL; AF222861; AAF37271.1; -.
InterPro; IPR001073; C1q.
                                                                                                                                                                                                                                                                                                   Sus scrota (Pig).
                                                                                                                                                                                                                                                                                                                          COL10A1
                                                                                                                                                                                                                                                                                                                                             Type X collagen.
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-ADIPOSE TISSUE:
MEDLINE-21232234; PubMed=11334417;
Hotta K, Funahashi T., Bodkin N.L.,
Hansen B.C., Matsuzawa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Cr.
Mammalia; Eutheria; Primates; Ca
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF404407; AAK92202.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Circulating concentrations of the adipocyte protein
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75; Conserv
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                 Cetartiodactyla;
                                                                                                                                                                                                                                                                         Chordata;
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21,
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                                                                                                                                  Arnbjerg
                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence up
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Pred. No. 1.7e-18;
Pred. No. 1.7e-18; Indels
                                                                                                                                                                                                                                               Craniata; Vertebrata; actyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Eutele Catarrhini; Cercopithecidae;
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                                                                                                                                    J.,
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                                                                                     carrying a
                                                                                                                                    Sorensen
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                                                                                                                                    C.M.,
                                                                                         dominant mutation
                                                                                                                                                                                                                                                   Sus
                                                                                                                                                                                                                                                                         Euteleostomi;
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                                                                                                                                    Jensen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                    H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Best Local
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Best Local :
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01-JUN-2002
01-JUN-2002
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BEG1.
Homo sapiens (Human).
Homo sapiens (Human).
Antonia; Metazoa; Chordata;
Antonia; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8TE71;
                                                                                                                                                                                                                                                                                       Aerbajinai W., Miller J.L.;
Submitted (JAN-2002) to the
EMBL; AY074490; AAL71549.1;
SEQUENCE 1077 AA; 120974
                          1014
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                                                                                                                                                                                                             34 GLPPDCSKCCHGDYS----FRGYQGPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 GYQGPPGPPGPPGIPGNHGNNGNNGATGHEG--AKGEKGDKGDLGP-----RGERGQHG
                                                                                                                                                       GATGHEGAKGEKGDKGDLGPRGERGQ-----
LFE
                                                                                                                             QVSSPE-RDNETFNSGDSGQGDSRSMTPVDVPVTNPAATILPVHVYP-LPQQMRVAFSAA
                        LMKNEEYLVSAYANDGAPDHETASNHAILQLFQGDQIWLRLHRGAIYGSSWKYSTFSGYL
                                    LMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRNGNGALHGDHQRFSTFAGFL 241
                                                                                                   LATHFS -- NONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSVMKHEDVEEVYVY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGKSDTSSNHAVLKLAKGDEVWLRM---GNGALHGDHQRFSTFAGFLL
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                                                                                                                                                                                                                                    72;
                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      675 AA; 65447 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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29.6%;
                                                                                                                                                                                                                                     43;
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                                                                                                                                                                                                                                 Score 273; DB 4;
Pred. No. 7e-16;
43; Mismatches 9
                                                                                                                                                                                                                                                                                        MW;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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les 87;
                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                     90;
                                                                                                                                                                                                                                                             Length 1077;
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RESULT

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Best Local S
Matches 73
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01-MAR-2001
01-DEC-2001
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Q9Z1K4;
01-MAY-1999
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   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                         protein)
                                                                                                                                                CDNA: FLJ22569
                                                                                                                                                                                                                                                                                                         Q9н667;
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Marks S.A., Lundmark C., Christersson C., Wurtz T., Odgren P.R.
Seifert M.F., MacKay C.A., Mason-Savas A., Popoff S.E.;
"Endochondral bone formation in toothless (osteopetrotic) rats:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01113; C10; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 GDYSFRGYQGPPGPPGPGIPGNHGNNGNNGATG----HEGAKGEKGDKGDLGPR---G 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNTVFSMYSYE--MKGKSDTSSNHAVLKLAKGDEVWLRMGN---GALHGDHQRESTFAGF
| :||:|: | : |:|:|: |: |:|:|:|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP--TMYTYDEYSKGYLDQASGSAIMELTENDQVWLQLPNAESNGLYSSEYVHSSFSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAYPAVGAPIPFDEILYNRQQHYDPRSGIFTCKIPGIYYFSYHI--HVKGTHVWVGLYKN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPGLPGPPGPPGPPSQAVIPDGFTKSGQRPRLSGMPLVSANQGVTGMPVSAFTVILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEPGIPGTRGPIGPPGIPGFPGSKGDPGKPGAPGPAGIVTKGLNGPAGPPGRPGPRCHTG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 AA; 30012 MW;
                                                                                                                                             (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
569 fis, clone HSIO2142 (Hypothetical 17.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 270; DB 11;
Pred. No. 2.8e-16;
34; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FF43B1548028813E CRC64;
                                                                                                                                                                                                                                                                                                                                                158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                                            AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Odgren P.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFMASLA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus
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RESULT
Q8TEJ5
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                                                           Query Match
Best Local :
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Best Local
                                                                                                                         Submitted (JAN-2002) to the EMBL; AK074129; BAB84955.1;
                                                                                                                                                  spleen."
                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                            Q8TEJ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01113; C1Q; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 158 AA; 17625 MW; 47
                                                                                                                                                                                                                                                                                                                                             Q8TEJ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-2001) to the EMBL; AK026222; BAB15398.1; EMBL; BC007520; AAH07520.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashi
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
                                                                                                  SEQUENCE
                                                                                                              NON_TER
                                                                                                                                                                                     TISSUE-SPLEEN;
                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                               FLJ00201
                                                                                                                                                                                                                                                                                           FLJ00201 protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001073; Clq. Pfam; PF00386; Clq; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                              "The nucleotide sequence of a
                                                                                                                                                                           Jikuya H.,
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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462 GPSGIPGLQGPAGPIGPQGLPGLKGEPGLPGPPG-EGRAGEPGTAGPTGPPGVPGSPGIT 520
                                                                                                                                                                                                                                                                                                                                                                                                                        140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 YPGIPPELQIAFMASLATHFS--NONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                 227
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                         GDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGE----
                                                                                                                                                                                                                                                                                                                                                                                                                       IYGSSWKYSTFSGYLLYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAPDHETASNHAILQLFQGDQIWLRLHRGA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YP-LPQQMRVAFSAARTSNLAPGTLDQPIVFDLLLNNLGETFDLQLGRFNCPVNGTYVFI 79
                                                  Similarity 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AUG-2000)
                                                                                              705 AA;
                                                                                                                                                                           Takano
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing project.";
000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                           J.,
                                                                                                 67430 MW; 07DB85A65A948ED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17625 MW; 47DB10EDD6DC9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.5%;
                                               18.9%; Score 258.5; DB 4; Length 705; 31.6%; Pred. No. 8.4e-15; 21ve 24; Mismatches 92; Indels 55
                                                                                                                                                                           Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                       157
                                                                                                                                                                                                                                                                                                                                                                                                                                               244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                         EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 266.5; DB 4
Pred. No. 2.7e-16;
                                                                                                                                                            long
                                                                                                                                                              Kikuno
ong cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                              R., Nagase T., clone isolated
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                                                                                                                                                                                                                                                                                                                   update)
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T.,
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RESULT 11
Q96D07
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Q8R002
ID Q8R00
AC Q8R00
DT 01-JU
R 01-JU
DT 01-JU
R Mamma
OC Eukar
OC Mamma
OC Eukar
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RN [1]
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Best Local
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Submitted (MAR-2002) to the EMBL, EMBL; BC023068; AAH23068.1; -.
EMBL; BC025174; AAH25174.1; -.
Hypothetical protein.
SEQUENCE 243 AA; 25420 MW; 4
 Q96D07;
01-DEC-2001
01-DEC-2001
                                               Q96D07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O8R002 PRELIMINARY; PRT
O8R002; PRELIMINARY; PRT
O1-JUN-2002 (TrEMBLrel. 21, Last
O1-JUN-2002 (TrEMBLrel. 21, Last
O1-JUN-2002 (TrEMBLrel. 21, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vi vov (III EMBLIEEL. 21, Last annotation update) Similar to DKF2P586B0621 protein (Hypothetical 25.4 Mus musculius (Monso)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   521
                                                                                                                                                                                                                                                                                                                              68
                                                                                                                                                                                                                                                                                                                                                                              11 LLALFFLPFCLCQDEYMESPQTGGLPPDCSK---CCHGDYSFRGYQGPPGPPGPPGIPGN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                      STFSGFLVY
                                                                                                                                                                                                        --LMHNGNTVFSMYSYEMKG---KSDTSSNHAVLKLAKGDEVWLRMGNG---ALHGDHQRF
                                                                                                                                                                                                                                                    ASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVY
                                                                                                                                               STFAGFLLF 243
                                                                                                                                                                            FDLVKNGQSIASFFQY-FGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTD
                                                                                                                                                                                                                                   RSESRVPPPADTPLPFDRVLLNEQGHFDPTTGKFTCQVPGVYYFAV----HATVYRASLQ
                                                                                                                                                                                                                                                                                              DGRDGRDGAPGAPGEKGEGGRPGLPGPRGEPGPRGEAGPMGAIGPAGECSVPPRSAFSAK
                                                                                                                                                                                                                                                                                                            HGNNGNNGATGHEGAKGEKGDKGDLGPRGE---RGQHGPKGEKGYPG---IPPELQIAFM 121
                                                                                                                                                                                                                                                                                                                                                       LLALLLLGLV-----SGSPPLDDNKIPSLCPGQ---PGLPGTPGHHGSQGLPGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMHNGNTVFSMYSYE--MKGKSDTSSNHAVLKLAKGDEVWLRM----GNGALHGDHQRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQHGPKGEKGYPGIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VALYKNNVPATYTYDEYKKGYLDQASGGAVLQLRPNDQVWVQMPSDQANG-LYSTEYIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVLTSPFPASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYFAY----HVHVKGTNVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPGPPGPPGAPGAFDETGIAGLHLPNGGVEGAVLGKGGKPQFGLGELSAHATPAFT 580
                                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
 (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                 18.8%; ilarity 32.5%; Conservative 3:
                                            PRELIMINARY;
                                                                                                                      233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
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19,
19,
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Created)
Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 257.5; DB 1
Pred. No. 2.9e-15;
3; Mismatches 100
                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498129CD051DB97B CRC64;
 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
                                            744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243
                                            AA
 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                             243;
                                                                                                                                                                                                                                                                                                                                                                                                                 35;
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RESULT 12
Q9D2V4
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Best Local S
Matches 78
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Q9D2V4;
01-JUN-2001
01-JUN-2001
01-JUN-2001
          STRAIN-C57BL/1.: TISSUE=KIDNEY;
MEDLINE-21085660; PubMed=11217851;
KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush :
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio J
Sakai K., Okido T., Furuno M., Anno H., Balarelli R., Barsh G.,
Inaka T., Boffelli D., Furuno M., Anno H., Balarelli R., Barsh G.,
 Sakai K.,
Blake J.,
                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013581; AAH13581.1; .
InterPro; IPR001073; C1q.
InterPro; IPR001087; Collagen.
Pfam; PP00386; C1q; 1.
Pfam; PP00386; C1q; 1.
Probom; PP01391; Collagen; 7.
Probom; PD000007; Collagen; 2.
PROSITE; PS01113; C1Q; UNKNOWN_1.
Collagen; Hypothetical protein.
Collagen; Hypothetical protein.
SEQUENCE 744 AA; 73364 MW; 2BC1B0955DE2C9A3 CRC64;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  COL8A1.
                                                                                                                                                                                                                                                                                                               Procollagen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Last annotation Hypothetical 73.4 kDa protein. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LUNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNG-----NNGATGHEGAKGE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAAGLYAGQYVHSSFSGYLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYHV--HCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSE 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGKPGALGPQGQPGLPGPPGPPGPPANMPPTPPPQGEYLPDMGLGIDGVKPPHAYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIPGD--QGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFPGIGKPGVAGLHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GALHGDHQRFSTFAGFLLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN- 224
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                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
, type VIII, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.8%; Score 257.5; 29.9%; Pred. No. 1.1
Bojunga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
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                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Carninci P.,
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; Murinae; Mus
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Best Local
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0921S8;
01-DEC-2001
01-DEC-2001
01-JUN-2002
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                                              Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC011061; AAH11061.1; ... MGD; MG1:88463; C018a1. InterPro; IPR001073; C1q. InterPro; IPR000087; Collagen. Pf00386; C1q: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0007; COMPLEMNTC1Q. SMART; SM00110; C1Q; 1. PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AK018742; BAB31383.1; -. MGD; MGI:88463; Col8al.
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Gustincich S., H
                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 7.
 Collagen.
SEQUENCE
                                                                                                                                        Strausberg
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                      Procollagen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
                                         Pfam; PF01391;
                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                        Pfam; PF01391; Collagen; 7. PROSITE; PS01113; ClQ; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGA------KGE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGVKPPHAYAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGDKGDLGPRGERGQHGPKGEKGYPGIP-----PELQI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIPGD--QGLQGPPGIPGIVGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGKPGVAGLHGP 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                         YHV--HCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQASGSAVLLLRPGDQVFLQMPSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTCEVPGVYYFA
                                                                                                                                                                                                                                                                                                                                                                                                                             -GALHGDHQRFSTFAGFLLF
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 744 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           744 AA;
                                                                                                                                                                                                                                                    (TIEMBLrel. 19, Created)
(TIEMBLrel. 19, Last sequence update)
(TIEMBLrel. 21, Last annotation update)
, type VIII, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFT 166
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                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                           (Mouse)
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                                                                                                                                                                                              Chordata;
Rodentia;
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  73621 MW;
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Pred. No. 1.2e-14;
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                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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 BF7A7FD79D8463AA CRC64;
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                                                                                                                                                                                                                                                                                                                            744 AA
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RESULT
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Best Local Similarity
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01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                   NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APM1
                                                                                                                                                                                                                                                                                      Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2001) to the EMELEMBL; AF417206; AAL09702.1; -. InterPro; IPR001073; C1, InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                 Kabir M., Ananthnarayan S., Ionut V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adiponectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q95J95
                                                                                                                                                                                                                                                                                                                                                                                       Dea M.K., Bergman R.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=ADIPOSE TISSUE;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9615;
                                                                                                                                                                                                                                                             ProDom; PD000007; Collagen; 1.
PROSITE; PS01113; C1Q; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                          "Regulation of Adiponectin gene expression in Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    723 AAGLYAGQYVHSSFSGYLLY 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               605
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                                                                               101 --HGPKGEKGYPGIPPEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGA------
                                                                                                                                    54 GP----PGPPGP-----PGIPGNHGNNGNNGATGHEGAKGEKGDKGD---LGPRGERGQ- 100
                                                                                                        1 GPGVLLPLPKGACPGWMAGIPGHPGHNGTPGRDGRDGTPGEKGEKGDPGLVGPKGDTGET 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YHV--HCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQASGSAVLLLRPGDQVFLQMPSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTCEVPGVYYFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGVKPPHAYAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGDKGDLGPRGERGQHGPKGEKGYPGIP-----PELQI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIPGD--QGLQGPPGIPGIVGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGKPGVAGLHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFT
DGTTGKFHCNIPGLYYFSYHITVY--LKDVKVSLYKKDKAMLFTYDQYQEKNVDQASGSV 178
                                                     GVTGVEGPRGFPGTPGRKGEPGESAYVHRSAFSVGLESRITVPNVPIRFTKIFYNLQNHY
                         DVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GALHGDHQRFSTFAGFLLF
                                                                                                                                                                 60;
                                                                                                                                                                           Similarity
                                                                                                                                                                                                                      194
194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (TrEMBLrel. 19,
1 (TrEMBLrel. 19,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.8%;
                                                                                                                                                                                                                      20890 MW; 3AA3D947D187AF9A CRC64;
                                                                                                                                                              18.1%; Score 247.5; 30.9%; Pred. No. 1.76 tive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 257; DB 11;
Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                               --- QIAFMASLATHESNQNSGIIFSSVETNIGNEF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194
                                                                                                                                                                                                                                                                                                                                                                                                       Kim
                                                                                                                                                                         1.7e-14;
                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                     S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
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                                                                                                                                                               71;
                                                                                                                                                                                                                                                                                                                                                              databases
                                                                                                                                                                                                                                                                                                                                                                          the fat-fed dog.";
                                                                                                                                                                                                                                                                                                                                                                                                       Van Citters G.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 744;
                                                                                                                                                                 Indels
                                                                                                                                                                                         Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
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                                                                                                                                                                 27;
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Query Match
Best Local Similarity
Tatches 71; Conserve
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Q9DCM6
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InterPro; IPR001073; Ciq.
InterPro; IPR001087; Collagen.
Pfam; PP00386; Ciq; 1.
Pfam; PP01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTCIQ.
SMART; SM00110; CiQ; 1.
PROSITE; PS01113; CiQ; 1.
PROSITE; PS01113; CiQ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK00265; BAB22262.1; -.
EMBL; BC002085; AAH02086.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H., Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., M., Casanibi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., M., Casanibi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., M., Casanibi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., M., Casanibi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., M., Casanibi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Pesole G., Quackenbu
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Complement component 1, q subcomponent, alpha polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; ature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=KIDNEY;
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                                                                                            154 RFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG--NTVFSMYSYEMKGKSDTSSNHAVLK 211
150 RFICAVPGFYYFNFQVISKWDL-CLFIKSSSGGQPRDSLSFSNTNNKGLFQVLAGGTVLQ 208
                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                  91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GYOGPPGPPGPPGNHGNNGNNGATG-HEGAKGEKGDKGD------LGP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                             31 GKDGAPGNPGRPGLKGERGEPGAAGIRTGIRGFKGDPGESGPPGKPGNVGLPGPSGP 90
                                                                                                                                                                                                                 LGDSGPQGLKGVKGNPGNIRDQPRPAFSAIRQNPMTLGNV-VIFDKVLTNQESPYQNHTG 149
                                                                                                                                                                                                                                                                                      RGERGQHGPKGEKGYPG-IPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.5%; Score 239.5; DB 11; Length 245; 33.2%; Pred. No. 1.2e-13; tive 26; Mismatches 94; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi; Muridae; Murinae; Mus
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Qy 212 LAKGDEVWLRM--GNGALHGDHQRFSTFAGFILF 243
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Search completed: January 15, 2003, 19:39:47 Job time : 94 secs

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Database
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                                                                                                                                                                                                                                                                                                                                                                     and is
                  290.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein search, using sw model
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1367
1 MLWRQLIYWQLLAL
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Goddard, Audrey Godowski, Paul

Eaton, Dan L.

Pan, James Gurney, Austin L. Stewart, Timothy A.

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ALIGNMENTS

PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/10/036,041
CURRENT FILING DATE: 2001-12-26 PRIOR APPLICATION NUMBER: 60/085579 TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3030R1C8 OR FILING DATE: 1998-12-22
OR APPLICATION NUMBER: 60/113430
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/113605
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/113621
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/114140
OR FILING DATE: 1998-12-23
OR FILING DATE: 1998-12-23
OR FILING DATE: 1998-12-23 OR APPLICATION NUMBER: 60/11552
OR FILING DATE: 1999-01-12
OR APPLICATION NUMBER: 60/116843
OR FILING DATE: 1999-01-22
OR APPLICATION NUMBER: 60/125774
OR FILING DATE: 1999-03-23
OR APPLICATION NUMBER: 60/125778 Watanabe, Colin K. Wood, William I. NUCLEIC

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FILING DATE: 2000-03-02
APPLICATION NUMBER: PCT/US00/14042
FILING DATE: 2000-05-22
APPLICATION NUMBER: PCT/US00/15264
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                                      PRIOR APPLICATION NUMBER: 60/112514
PRIOR TILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
                                                                                                 PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
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OR APPLICATION NUMBER: 60/138166
OR FILING DATE: 1999-06-08
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OR FILING DATE: 1999-07-20
OR APPLICATION NUMBER: 60/146970
OR FILING DATE: 1999-08-03
OR APPLICATION NUMBER: 60/162506
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DR FILING DATE: 1999-04-27
DR APPLICATION NUMBER: 60/131291
DR FILING DATE: 1999-04-27
DR APPLICATION NUMBER: 60/132371
DR FILING DATE: 1999-05-04
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APPLICATION NUMBER: 09/869599
FILING DATE: 2001-06-29
APPLICATION NUMBER: 09/908,827
                      APPLICATION NUMBER: PCT/US99/30720 FILING DATE: 1999:12-22 APPLICATION NUMBER: PCT/US00/05601 FILING DATE: 2000-03-01
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APPLICATION NUMBER: PCT/US99/28551
FILING DATE: 1999-12-02
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FILING DATE: 1999-05-14
APPLICATION NUMBER: 09/380142
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APPLICATION NUMBER: PCT/US99/10733
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FILING DATE: 1999-05-04
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FILING DATE: 1999-04-21
APPLICATION NUMBER: 60/131270
FILING DATE: 1999-04-27
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FILING DATE: 1999-04-05
APPLICATION NUMBER: 60/129122
FILING DATE: 1999-04-13
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FILING DATE: 1999-03-23
APPLICATION NUMBER: 60/125778
FILING DATE: 1999-03-23
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                                                                                                   APPLICANT: Desnoyers, Luc
APPLICANT: EatOn, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin
APPLICANT: Gurney, Austin
APPLICANT: Pan, James
APPLICANT: Stewart, Timoth
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                                                      APPLICANT:
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APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3030R1C5
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FILING DATE: 2000-08-24
APPLICATION NUMBER: PCT/US00/32678
FILING DATE: 2000-12-01
APPLICATION NUMBER: PCT/US00/34956
FILING DATE: 2000-12-20
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APPLICATION NUMBER: PCT
FILING DATE: 2000-05-22
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FILING DATE: 2000-06-02
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246; Conserv
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Godowski, Paul J.
                                                                      Watanabe, Colin | Wood, William I.
                                                                                                                                       Gurney, Austin L.
                                                                                                     Stewart, Timothy A
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PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
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CURRENT FILING DATE: 2001-12-26
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OR FILING DATE: 1998-12-22
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OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/113605
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/113621
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/114140
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/11555
OR APPLICATION NUMBER: 60/11555
OR FILING DATE: 1998-12-23
DR APPLICATION NUMBER: 09/747259
DR FILING DATE: 2000-12-20
DR FILING DATE: 2001-03-22
DR FILING DATE: 2001-03-22
DR APPLICATION NUMBER: 09/854208
DR APPLICATION NUMBER: 09/854208
DR APPLICATION NUMBER: 09/854280
DR APPLICATION NUMBER: 09/854280
DR FILING DATE: 2001-05-10
DR APPLICATION NUMBER: 09/874503
DR FILING DATE: 2001-05-05
DR APPLICATION NUMBER: 09/869599
DR APPLICATION NUMBER: 09/869599
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APPLICATION NUMBER: 60/132383
FILING DATE: 1999-05-04
APPLICATION NUMBER: 60/135750
FILING DATE: 1999-05-25
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FILING DATE: 1999-05-14
APPLICATION NUMBER: 09/380142
FILING DATE: 1999-08-25
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FILING DATE: 1999-06-08
APPLICATION NUMBER: 60/144791
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APPLICATION NUMBER: 60/127706
FILING DATE: 1999-04-05
APPLICATION NUMBER: 60/129122
FILING DATE: 1999-04-13
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FILING DATE: 1999-10-29
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FILING DATE: 1999-04-27
APPLICATION NUMBER: 60/131272
FILING DATE: 1999-04-27
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FILING DATE: 1999-04-21
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PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Homo Sapien
US-10-036-342-2
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Best Local Similarity
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IOR FILING DATE: 2000-08-24

IOR APPLICATION NUMBER: PCT/US00/32678

IOR FILING DATE: 2000-12-01

IOR APPLICATION NUMBER: PCT/US00/34956

IOR FILING DATE: 2000-12-20

IOR APPLICATION NUMBER: PCT/US01/06520

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APPLICATION NUMBER: PCT/US00/15264
FILING DATE: 2000-06-02
APPLICATION NUMBER: PCT/US00/23522
FILING DATE: 2000-08-23
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FILING DATE: 2000-03-01
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: 2000-03-02
APPLICATION NUMBER: PCT/US00/14042
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FILING DATE: 1999-05-14
APPLICATION NUMBER: PCT/US99/28551
FILING DATE: 1999-12-02
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LLFETK 246
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                                                                                                                                          YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF
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2001-06-29
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Pred. No. 9.9e-112;
Pred. No. 9.9e-112;
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RESULT 4
US-09-776-976-4
; Sequence 4, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim

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; SOFTWARE: Patent.pm
; SEQ ID NO 4
; LENGTH: 247
; TYPE: PRT
; ORGANISM: mus musculus
US-09-776-976-4
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CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
                                        SOFTWALL SEQ ID NO 4
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Best Local :
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PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
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TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10
CURRENT FILING DATE: 2001-01-10
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APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
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PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
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SOFTWARE: Patent.pm
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TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
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ORGANISM: mus musculus
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Best Local Similarity
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PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 7
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PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
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TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US6.CIP
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                                                                                                                         64 IPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGER----GQHGPKGEKGYPGIPPE-----
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EAAYMYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHIT 168
                                       ----LQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMM 170
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Yen, Frances
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31.5%; Pred. No. 1.5e-18;
tive 40; Mismatches 102;
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ANTIBODIES THAT BIND AN
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROT
FILE REFERENCE: 97-30D1
CURRENT APPLICATION UNMBER: US/09/911,176B
CURRENT FILING DATE: 2001-07-23
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09776976 Patent No. US20020037849Al
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LENGTH: 244
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 PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
                                                                                                             CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
                                                                                                                                              APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
                                                                                                                                                                                                                          APPLICANT: Fruebis, Joachim APPLICANT: Erickson, Mary 1
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NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version
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Similarity 34.5%;
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Pred. No. 1.7e-18;
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; ORGANISM: Homo sapiens US-09-758-055-6
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SEQ ID NO 6
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SEQ ID NO 6
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Best Local Similarity
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APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: 0B63 Globular Head and Uses Thereof for Decreasing Body Mass
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PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
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CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10
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TYPE: PRT
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TYPE: PRT
ORGANISM: Homo sapiens
                                                    148 FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNH 207
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les 76; Conserv
YDGSTGKFHCNIPGLYYFAYHITVY--MKDVKVSLFKKDKAMLFTYDQYQENNVDQASGS
                                                                                                     TGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNH 142
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Pred. No. 1.7e-18;
5; Mismatches 78
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201 VLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240

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; ORGANISM: Homo
US-09-909-547-6
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CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/776,976
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR APPLICATION NUMBER: US 06/299,881
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                 Sequence 2, Application US/09776976
Patent No. US20020037849A1
GENERAL INFORMATION:
APPLICANT: Fruebis, Joachim
APPLICANT: Erickson, Mary Ruth
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FILE REFERENCE: 76.US4.REG
CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
                                                                    APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing
FILE REFERENCE: 76.US4.REG
                                                                                                                                APPLICANT:
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SOFTWARE: Patent.pm
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TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
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Pred. No. 1.7e-18;
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                                                                                                                                                                           SOFTWARE: Patent.pm
SEQ ID NO 2
LENGTH: 247
TYPE: PRT
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Best Local
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CURRENT FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
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SOFTWARE: Patent.pm
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TYPE: PRT
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                                                                   Local Similarity 31.2 nes 81; Conservative
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LLLQALLFLLILP-SHAEDDVTTTEELAPALVPPPKGTCA---
                               LIYWQLLALFFLPFCLCQDEYMESPQTGG--LPPDCSKCCHGDYSFRGYQGPPGPPGPPG 63
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Pred. No. 1.9e-18;
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tches 99;
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US-09-909-547-2
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US-09-909-547-2
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PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
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LENGTH: 247
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Patent No. US20020091080A1
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CURRENT FILING DATE: 2001-07-19
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IITLE OF INVENTION: OBG3 Globular Head and
ILE REFERENCE: 76.US6.CIP
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224 HNGLYADNVNDSTFTGFLLF 243
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Local Similarity 31.2%;
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                                                                    HITVY -- MKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGD
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Pred. No. 1.9e-18;
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US-09-992-598-47; Sequence 47; Application US/09992598
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APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER:
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
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                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/087106 FILING DATE: 1998-05-28
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FILING DATE: 1998-02-25
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Baker, Kevin P.
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Stewart, Timothy A.
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-KGEMGSPGAP--CQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAA
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APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19

APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-19

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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18

APPLICATION NUMBER: 60/0

APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22

APPLICATION NUMBER:

60/090246

FILING DATE: 1998-06-19

APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17

APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17

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FILING DATE: 1998-06-16 APPLICATION NUMBER: FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-16

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APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876

FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088861

APPLICATION NUMBER: 60/ APPLICATION NUMBER:

60/088858 60/088826 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-10

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APPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10

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APPLICATION NUMBER: 60/088217

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NUMBER: 60/088030

APPLICATION NUMBER:

1998-06-04

FILING DATE: APPLICATION NUMBER:

1998-06-05

60/088202 60/088167 60/088326 60/088033

APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16

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RESULT 15
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CURRENT APPLICATION NUMBER: US/09/989,293A

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/049787

PRIOR APPLICATION NUMBER: 60/062250

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PRIOR APPLICATION NUMBER: 60/065186
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Botstein, David
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P. Mickey
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PRIOR APPLICATION NUMBER: 60/088734
              OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/08
OR FILING DATE: 1998-06-18
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60/090349

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-22

NUMBER: 60/089952

1998-06-

FILING DATE: 1998-06-

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                                                                  Query Match 21.3%; Score 290.5; DB 9
Best Local Similarity 28.8%; Pred. No. 3.3e-18;
Matches 78; Conservative 34; Mismatches 96
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OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090557
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090676
OR APPLICATION NUMBER: 60/090678
OR APPLICATION NUMBER: 60/090678
OR APPLICATION NUMBER: 60/090690
9 WQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCC----
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090862
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090429
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Search completed: January 15, 2003, 19:45:53 Job time: 245 secs

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Age.
9,
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Alignment Scores: Pred. No.:

Sequence 1123

BP;

277

A; 266

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321 G;

258 H

Length:

1123

235pp; English.

The invention relates to novel nucleic acid sequences derived from rat clearmal papilla, human keratinocytes and meonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhabit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle to treat growth and developmental defects, skin wounds and hair follicle CC disorders. Sequences AA261606-261832 represent cDNA sequences derived CC AA261606-261649, AA261725-261765, AA261802-261811 and AA261826 encode CC CAA261832 represent cDNA sequences derived CC CAA2618381 and AA261826 encode CC CAA261839 encode proteins with an N-terminal signal sequence, indicating that the proteins CC are secreted. Sequences AA261650-261668, AA261766-261780, AA261812-261817 and AA261827-261829 encode proteins with one or more putative transmembrane domains.

Sequence 1123 ₿₽; 277 A; 266 Ç 321 <u>લ</u> 258 Η, other;

밁 Š õ δã Вb δÃ Percent Similarity:
Best Local Similarity:
Query Match: ρ 밁 Ş 밁 δÃ 밁 В 뫄 δõ 밁 Ş Ş δõ 밁 B US-10-036-041-2 (1-246) Мо.: 201 181 660 161 600 141 540 121 480 101 420 360 300 240 180 61 41 81 21 Н GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaproValSer 160 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140 GGGGCCAAGGGTGAGAAAGGACAAAAGGCGACCTGGGGGCCTCGAGGGGAACGGGGCAG CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA AAGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCAGACTGCAGC GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGGCCCCCGTATCA ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC 3.36e-95 1311.00 97.15% 95.93% 95.90% 21 x AAZ61633 (1-1123)Length:
Matches:
Conservative: Mismatches: Indels: 419 719 539 479 100 , 8 359 60 599 299

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RESULT 11
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                                          dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, cand mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cc cancer and neurological diseases: The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cc cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle clasorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived AAZ616049, AAZ61725-Z61765, AAZ61802-Z61811 and AAZ61826 encode conserved. Sequences AAZ61609-Z61668, AAZ61766-Z61780, AAZ61817-Z61817 are secreted. Sequences AAZ61650-Z61668, AAZ61766-Z61780, AAZ61817-Z61817 and AAZ61827-Z61839 encode proteins with one or more putative
                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 137; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides useful for including wounds and cancer -
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09-NOV-1998;
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developmental disorder; skin wound; hair follicle disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding rat skin cell secreted protein, SEQ ID NO:203
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                                                                                                                                                                                                                                                                                                                                  The invention relates to novel nucleic acid sequences derived from rat
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98US-0188930
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RESULT 12
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CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu

GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGACCTGGGGGCCTCGAGGGGAACGGGGGCAG

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CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGC LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer

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Percent Similarity:
Best Local Similarity:
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CURRENT APPLICATION NUMBER: US/09/188,930A; CURRENT FILING DATE: 1998-11-09; NUMBER OF SEQ ID NOS: 348; SOFTMARE: FastSEQ for Windows Version 3.0; SEQ ID NO 203; LENGTH: 1123; TYPE: DNA; ORGANISM: Rat US-09-188-930-203
                                                                                               APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions In
TITLE OF INVENTION: and Methods For
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US-09-188-930-203
   Alignment
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Patent No. 6150502
GENERAL INFORMATION:
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isola
TITLE OF INVENTION: and Methods For Th
                                                            Sequence 217, Applic Patent No. 6150502 GENERAL INFORMATION:
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